

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 04/09/03  
Searcher: BEVERLY E. 994  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 28  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

### Search Site

\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_\_ N.A. Sequence  
\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG Suite  
\_\_\_\_\_ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
\_\_\_\_\_ DARC/Questel  
\_\_\_\_\_ Other 0000

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STIC-Biotech/ChemLib

89679

From: Monshipouri, Maryam  
Sent: Monday, March 24, 2003 9:47 AM  
To: STIC-Biotech/ChemLib  
Subject: case #09/719,748

Please **interference** search SEQ ID NO:1-2,  
residues 1022-1141 of SEQ ID NO:1 ;and  
residues 13-275 of SEQ ID NO:2.

Thank you.

**Maryam Monshipouri Ph.D.**  
**Primary Examiner**  
Art Unit 1652  
Mail box No. 10D01

Point of Contact  
Beverly Shears  
Technical Info. Specialist  
CM1 1E05 Tel: 308-4994

RECEIVED  
MAR 24 2003  
(STIC)

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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Monish/pour  
09/17/19748  
Seq. IDs 172  
Page 1

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 19:24:37 ; Search time 5382.24 Seconds  
(without alignments)  
8137.548 Million cell updates/sec

Title: US-09-719-748-1

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Result				SUMMARIES			
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3	1742	100.0	1742	28	US-09-719-748-1	Sequence 1, Appl1	
4	1730.4	99.3	2235	23	US-09-606-776-3799	Sequence 3799, Ap	
5	1728.8	99.2	2235	25	US-09-649-163-9895	Sequence 9895, Ap	
6	1728.8	99.2	2235	25	US-09-652-917-3775	Sequence 3775, Ap	
7	1728.8	99.2	2235	27	US-09-698-010-12235	Sequence 12235, A	
8	1728.8	99.2	2235	27	US-09-698-013-6041	Sequence 6041, Ap	
9	1715.8	98.5	1970	71	US-60-278-232-3329	Sequence 3329, Ap	
10	1042.2	59.8	1864	29	US-09-757-982-10	Sequence 10, Appl	
11	1032.4	59.3	1732	80	US-60-360-207-7361	Sequence 3361, Ap	
12	1019.2	58.5	1512	25	US-09-649-163-7647	Sequence 7647, Ap	
13	1019.2	58.5	1512	25	US-09-652-816-8022	Sequence 8022, Ap	
14	1019.2	58.5	1512	25	US-09-652-913-8169	Sequence 8169, Ap	
15	1019.2	58.5	1512	25	US-09-652-917-2793	Sequence 2793, Ap	
16	1017.6	58.4	1451	16	US-09-277-214-116	Sequence 176, App	
17	1017.6	58.4	1451	33	US-09-891-825-176	Sequence 9265, App	
18	1015	58.3	1253	1	PCT-US01-08631-9265	Sequence 8371, Ap	
19	952	54.6	1198	25	US-09-652-914-8371	Sequence 450, App	
20	750.2	43.1	830	30	US-09-760-446-450	Sequence 450, App	
21	750.2	43.1	830	42	US-10-206-664-450	Sequence 450, App	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22 720.8 41.4 825 30 US-09-760-443-677 Sequence 677, App
23 720.8 41.4 825 30 US-09-760-446A-1075 Sequence 1075, App
24 720.8 41.4 825 42 US-10-206-664-1075 Sequence 1075, App
25 720.8 41.4 825 42 US-10-212-054-677 Sequence 677, App
26 575.2 33.0 580 21 US-09-540-212A-62505 Sequence 62505, A
27 545 31.3 553 65 US-60-213-178-1077 Sequence 1077, App
28 517.2 29.7 1096 25 US-09-644-868-8422 Sequence 8422, App
29 517.2 29.7 1096 25 US-09-644-871-8496 Sequence 8496, App
30 517.2 29.7 1096 25 US-09-652-125A-8631 Sequence 8631, App
31 517.2 29.7 1096 25 US-09-652-126-7114 Sequence 7114, App
32 517.2 29.7 1096 25 US-09-652-913-9613 Sequence 9613, App
33 517.2 29.7 1096 25 US-09-652-916-8397 Sequence 8397, App
34 517.2 29.7 1096 23 US-09-652-916-2683 Sequence 2683, App
35 517.2 29.7 1096 23 US-09-611-526-2874 Sequence 2874, App
36 517.2 29.7 2201 71 US-60-278-258-4326 Sequence 4326, App
37 517.2 29.7 2201 71 US-60-172-373-4473 Sequence 4473, App
38 517.2 29.7 2384 25 US-09-606-776-3765 Sequence 3765, App
39 517.2 29.7 2384 25 US-09-652-125A-9484 Sequence 9484, App
40 517.2 29.7 2387 25 US-09-652-126-8978 Sequence 8978, App
41 517.2 29.7 2387 25 US-09-652-916-10429 Sequence 10429, App
42 517.2 29.7 2387 25 US-09-652-917-3657 Sequence 3657, App
43 517.2 29.7 2387 25 US-09-652-918-8294 Sequence 8294, App
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## ALIGNMENTS

RESULT 1  
PCT-US99-13411-1

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/ SEQUENCE INFORMATION:
/ APPLICANT: KIMCHI, Adi
/ APPLICANT: MCINNIS, A., Patricia
/ APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
/ TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
/ FILE REFERENCE: KIMCHI2
/ CURRENT APPLICATION NUMBER: PCT/US99/13411
/ CURRENT FILING DATE: 1999-06-15
/ EARLIER APPLICATION NUMBER: 60/089,294
/ EARLIER FILING DATE: 1998-06-15
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1742
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (62)..(1141)
PCT-US99-13411-1

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Query Match 100.0%; Score 1742; DB 1; Length 1742;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACCGCGGACCTGAGCCTCCGCGGATTTGATGTTCCAGGCTTCATGAGAGTCCAAA 60
DB 1 GACCGCGGACCTGAGCCTCCGCGGATTTGATGTTCCAGGCTTCATGAGAGTCCAAA 60
QY 61 CATGAGCATTTCAAGCAGAGAGAGTGAAGACTTTTATGACATCGAGAGAGAGCTGGG 120
DB 61 CATGAGCATTTCAAGCAGAGAGAGTGAAGACTTTTATGACATCGAGAGAGAGCTGGG 120
QY 121 GAGTGGCAGTTTGCATCGTGAAGAAAGTCCCGGAGAAAGCAAGGAGCTTGATGTC 180
DB 121 GAGTGGCAGTTTGCATCGTGAAGAAAGTCCCGGAGAAAGCAAGGAGCTTGATGTC 180
QY 181 AGCCAAATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 AGCCAAATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

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QY 241 GATCGAGCGGAGAGTGAAGTCTCGGAGAGTGTGACCAATATGATCATCGCTGCA 300
DB 241 GATCGAGCGGAGAGTGAAGTCTCGGAGAGTGTGACCAATATGATCATCGCTGCA 300
QY 301 CGAGCTCTATGAGAACCGGACCGAGCTGTGACATCTCTTGAAGTATGCTCGAGAGAG 360
DB 301 CGAGCTCTATGAGAACCGGACCGAGCTGTGACATCTCTTGAAGTATGCTCGAGAGAG 360
QY 361 GCTCTTGAATTTCTGCGCCAGAGAGAGTCACTGATGAGAGAGAGAGAGAGAGAGAG 420
DB 361 GCTCTTGAATTTCTGCGCCAGAGAGAGTCACTGATGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TAAGCAGATCTGATGAGAGTGAATCTTCAACAAAGAAATTTGCTACCTTATGCT 480
DB 421 TAAGCAGATCTGATGAGAGTGAATCTTCAACAAAGAAATTTGCTACCTTATGCT 480
QY 481 CAAGCCAGAAATATATATGTTTGAACAAAGAAATTTCCATTCACATCAAGCTGAT 540
DB 481 CAAGCCAGAAATATATATGTTTGAACAAAGAAATTTCCATTCACATCAAGCTGAT 540
QY 541 TGACTTTGCTGTGCTGCTCAAGAAATTTGAACTGAGAGAGAGAGAGAGAGAGAGAG 600
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QY 661 GTGAGAGATGAGGCTGCTCACTGATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAG 720
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QY 721 CACGAGCAGAGAACTATGCTCACTGATCTTCAAGTGAAGAGAGAGAGAGAGAGAG 780
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QY 781 CTTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 CTTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CCGGAAAGCGCTCACTGATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 CCGGAAAGCGCTCACTGATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 CCAGCAAGCCATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CCAGCAAGCCATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TGTCCGAGGCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TGTCCGAGGCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 CTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 CTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 CACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 CTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 CTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 GAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 GAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 GGCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 GGCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

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Qy	1321	GGCGTGTCTCTGTGAGAGAGGCTCCAGCATTCGCAAGCTCTTAATTCCTCATTTAAATGG	1380
Db	1321	GGCTGTCTTCTGTGAGAGAGGCTCCAGCATTCGCAAGCTCTTAATTCCTCATTTAAATGG	1380
Qy	1381	GCTTTCCTCTGTCTGTGCAATCTCCAGAGTGTGGGAGGTGGGAGTGTGGACTTAAAGAAACAAT	1440
Db	1381	GCTTTCCTCTGTCTGTGCAATCTCCAGAGTGTGGGAGGTGGGAGTGTGGACTTAAAGAAACAAT	1440
Qy	1441	ATTAAGGACATCTCATCATCAACAGGGGTGAAGTCAAGATGAAGCAGGCTCTTCAACAGG	1500
Db	1441	ATTAAGGACATCTCATCATCAACAGGGGTGAAGTCAAGATGAAGCAGGCTCTTCAACAGG	1500
Qy	1501	CTGAGGGGGTTCAAAACCAAGCTGGCCAAATAACACAGAGACAGAGTCTCTCCCA	1560
Db	1501	CTGAGGGGGTTCAAAACCAAGCTGGCCAAATAACACAGAGACAGAGTCTCTCCCA	1560
Qy	1561	TTGGGACAGGGGTGATTTGAGAAAGTGAACCTTGGGTGTGAGGAGCCAAATCCTGTGACCT	1620
Db	1561	TTGGGACAGGGGTGATTTGAGAAAGTGAACCTTGGGTGTGAGGAGCCAAATCCTGTGACCT	1620
Qy	1621	CCCAAGAACCATGGAAGCCAGAGACGTCAAGCTGACCAACACCTTCAGA	1680
Db	1621	CCCAAGAACCATGGAAGCCAGAGACGTCAAGCTGACCAACACCTTCAGA	1680
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Db	1681	CCATTGCTGGCCGCGCATGTGTGAATTTTGTCTCAATTTTAAATCTTCGGGTTTAACTGG	1740
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Db	1741	AA 1742	

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RESULT 3
US-09-719-748-1
; Sequence 1, Application US/09719748
; GENERAL INFORMATION:
; APPLICANT: KIMCHI, Adi
; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
; FILE REFERENCE: KIMCHI2a
; CURRENT APPLICATION NUMBER: US/09/719,748
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/089,294
; PRIOR FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (62)..(1141)
US-09-719-748-1

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QY	1	GACCGGCGAGCTCAGCCCTCCGCGCATTTGATGTTCACAGGCTCAATGAGAGTCCAAA	60	
Db	1	GACCGGCGAGCTCAGCCCTCCGCGCATTTGATGTTCACAGGCTCAATGAGAGTCCAAA	60	
QY	61	CATGAGCATTCAAGCAGCAGAGAGTGGAGACTTTTATGACATCGAGAGAGGAGCTGGG	12	
Db	61	CATGAGCATTCAAGCAGCAGAGAGTGGAGACTTTTATGACATCGAGAGAGGAGCTGGG	12	
QY	121	GAGTGCCCAATTTGCCATGTGAAGAGTGCAGGAGAGAGGCACTGGAGTATGC	18	
Db	121	GAGTGCCCAATTTGCCATGTGAAGAGTGCAGGAGAGAGGCACTGGAGTATGC	18	

Qy	181	AGCCAGTTCATCAAGAGCGGCAAGGCCGGGCGAGCCGCGGTGTGAGCCGGGAGGA	240
Db	181	AGCCAGTTCATCAAGAGCGGCAAGGCCGGGCGAGCCGCGGTGTGAGCCGGGAGGA	240
Qy	241	GATGAGCGGGAGGCTGAGCATCTCTGGCGGCAAGTGTCTGACCAACAATGTCTACGCTGCA	300
Db	241	GATCAGCGGAGGTGAGCATCTCTGGCGGCAAGTGTCTGACCAACAATGTCTACGCTGCA	300
Qy	301	CGACGCTTATGAGAAACCGCACCGACCGTGTGTACATCTCTGAGCTGTGTGAGAGGA	360
Db	301	CGACGCTTATGAGAAACCGCACCGACCGTGTGTACATCTCTGAGCTGTGTGAGAGGA	360
Qy	361	GCTCTTCGATTTCCGCGCCGAGAGAGTCACTGAGTGAAGAGAGGCCACACGCTTCAT	420
Db	361	GCTCTTCGATTTCCGCGCCGAGAGAGTCACTGAGTGAAGAGAGGCCACACGCTTCAT	420
Qy	421	TAGAGAGATCTCGATGAGGAGTGAATCTTCAACAACAAGAAATTGCTACCTTATCT	480
Db	421	TAGAGAGATCTCGATGAGGAGTGAATCTTCAACAACAAGAAATTGCTACCTTATCT	480
Qy	481	CAAGCCAGAAACATTATGTTGTAGACAAGAAATTTCCATTCACACATCAAGCTGAT	540
Db	481	CAAGCCAGAAACATTATGTTGTAGACAAGAAATTTCCATTCACACATCAAGCTGAT	540
Qy	541	TGACTTGGTCTGCTCAGCAAAATGAAATGAGAGTTGAATTTTAAGAAATTTTTGGAC	600
Db	541	TGACTTGGTCTGCTCAGCAAAATGAAATGAGAGTTGAATTTTAAGAAATTTTTGGAC	600
Qy	601	GCCGGAATTTGTGCTCCCGAGAAATTGTGAATCAACAGCCCTCGGAGTGTGAGGCTGACAT	660
Db	601	GCCGGAATTTGTGCTCCCGAGAAATTGTGAATCAACAGCCCTCGGAGTGTGAGGCTGACAT	660
Qy	661	GTCGAGCATAGGCGTATCATCCTAATCTCTTAAAGTGAACAATCCCTCTTCTGGGAGA	720
Db	661	GTCGAGCATAGGCGTATCATCCTAATCTCTTAAAGTGAAGATCCCTCTTCTGGGAGA	720
Qy	721	CAGCAACAGAGAAACCTGGCAAAATATCAATCAGTGAAGTTTACGACTTTGATGAGAAATT	780
Db	721	CAGCAACAGAGAAACCTGGCAAAATATCAATCAGTGAAGTTTACGACTTTGATGAGAAATT	780
Qy	781	CTTACGCAATACGAGCGAGCTGGCCAAAGCACTTTATTCGAAAGCTTCTGTAAAGAGAC	840
Db	781	CTTACGCAATACGAGCGAGCTGGCCAAAGCACTTTATTCGAAAGCTTCTGTAAAGAGAC	840
Qy	841	CCGGAACCGTCTCAATCCAAAGAGGCTTCAGACACCCCTGGATCACGCGGTGACAA	900
Db	841	CCGGAACCGTCTCAATCCAAAGAGGCTTCAGACACCCCTGGATCACGCGGTGACAA	900
Qy	901	CCAGAGACCAATGTCGACCGGAGTGTGTGTCATCTGAGAACTTCAGAAAGCAATGA	960
Db	901	CCAGAGACCAATGTCGACCGGAGTGTGTGTCATCTGAGAACTTCAGAAAGCAATGA	960
Qy	961	TGTCGCGAGCGGTGGAAGCTTTCTTCAGATGTGTCTCTGTGCAACCACTCAACCGG	1020
Db	961	TGTCGCGAGCGGTGGAAGCTTTCTTCAGATGTGTCTCTGTGCAACCACTCAACCGG	1020
Qy	1021	CTTCGCTGATGAAGAGTGTGACCTTGAGGCGGATGAGGACCTTGAGAACTGTGAGATGA	1080
Db	1021	CTTCGCTGATGAAGAGTGTGACCTTGAGGCGGATGAGGACCTTGAGAACTGTGAGATGA	1080
Qy	1081	CACCTGAGAGGACATGCGCAGAGAGAAAGCCCTTCACCAAGAGAGAGACACCACTC	1140
Db	1081	CACCTGAGAGGACATGCGCAGAGAGAAAGCCCTTCACCAAGAGAGAGACACCACTC	1140
Qy	1141	CTAACCTGAGCTGACCTGACGAGTGGCCGACAGGAGGTTTGGGCCAGCGGGGCTCCCTTCT	1200
Db	1141	CTAACCTGAGCTGACCTGACGAGTGGCCGACAGGAGGTTTGGGCCAGCGGGGCTCCCTTCT	1200
Qy	1201	GTCGAGACTTTTGAGACCACTGACCACTGACCACTCCGGGCGTCTGAGACACTTTGCAAGA	1260
Db	1201	GTCGAGACTTTTGAGACCACTGACCACTGACCACTCCGGGCGTCTGAGACACTTTGCAAGA	1260
Qy	1261	GAGATGGGCCCAAGAAATTCAGAAAGCTTTGACGCGCAAGCCAGAGAACCTTGGAGCTGT	1320



Db 1261 GAGATGGGCCCCAGGAATTCAGAAAGCTTGGAGCAAGCCAGGAGACCTGGGGAGCTGT 1320  
Qy 1321 GGCCTGCTCTGTGGAGAGAGCTCCAGCATTCCTCAAAAGCTCTTAATTCCTCAATAATGG 1380  
Db 1321 GGCCTGCTCTGTGGAGAGAGCTCCAGCATTCCTCAAAAGCTCTTAATTCCTCAATAATGG 1380  
Qy 1381 GCTTTCCTCTGTGCTCCTCCTCAGAGTCTGGGGTGGAGTGTGGACTTAAGAAAAACAT 1440  
Db 1381 GCTTTCCTCTGTGCTCCTCCTCAGAGTCTGGGGTGGAGTGTGGACTTAAGAAAAACAT 1440  
Qy 1441 ATAAAGCATTCCTCATATCATCGGGGTGAAGGTCAAGTAAGGACCTTCTTCAACGG 1500  
Db 1441 ATAAAGCATTCCTCATATCATCGGGGTGAAGGTCAAGTAAGGACCTTCTTCAACGG 1500  
Qy 1501 CTGAGGGGGTTCAGAACAGAGCTGGCCAAAATTACACAGAGAGACAGAGCTCCCA 1560  
Db 1501 CTGAGGGGGTTCAGAACAGAGCTGGCCAAAATTACACAGAGAGAGAGAGCTCCCA 1560  
Qy 1561 TTGGGAACAGGGGTATTGAGGAAGTGAACCTTGGGTGAGGGAACAATCCTGTGACT 1620  
Db 1561 TTGGGAACAGGGGTATTGAGGAAGTGAACCTTGGGTGAGGGAACAATCCTGTGACT 1620  
Qy 1621 CCCAGAACATGGAAGCCAGAGCTCAGGCTGACCAACCTCAGACCTTCTGAAGCAGC 1680  
Db 1621 CCCAGAACATGGAAGCCAGAGCTCAGGCTGACCAACCTCAGACCTTCTGAAGCAGC 1680  
Qy 1681 CCATTGCTGGCCCGCCATGTTGTAATTTTGCATTTTAACTTCTGGTTAACTCG 1740  
Db 1681 CCATTGCTGGCCCGCCATGTTGTAATTTTGCATTTTAACTTCTGGTTAACTCG 1740  
Qy 1741 AA 1742  
Db 1741 AA 1742

RESULT 4  
US-09-606-776-3799  
; Sequence 3799, Application US/09606776  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Meyer, Paul  
; APPLICANT: Geary, David P.  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1129-001  
; CURRENT APPLICATION NUMBER: US/09/606,776  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: 60/141,578  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/141,379  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: 60/141,138  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: 60/141,581  
; NUMBER OF SEQ ID NOS: 5415  
; SOFTWARE: FaSeq for Windows Version 3.0  
; SEQ ID NO 3799  
; LENGTH: 2235  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-606-776-3799

Query Match 99.3%; Score 1730.4; DB 23; Length 2235;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1734; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ACCGGGAGAGCTCAGGCTCCGCGGATGTAATTCAGGAGCTCAATAGAGATCCAAAC 61  
Db 1 ACCGGGAGAGCTCAGGCTCCGCGGATGTAATTCAGGAGCTCAATAGAGATCCAAAC 60

Qy 62 ATGAGCATTCAAGCAGAGAGGTGAGACTTTTATGACATCGAGAGAGAGCTGGGG 121  
Db 61 ATGAGCATTCAAGCAGAGAGAGGTGAGACTTTTATGACATCGAGAGAGAGCTGGGG 120  
Qy 122 AGTGCCCATTTTGGCATGCTGAAGAGTCCGGGAGAGAACACAGGGCTTGAATATCA 181  
Db 121 AGTGCCCATTTTGGCATGCTGAAGAGTCCGGGAGAGAACACAGGGCTTGAATATCA 180  
Qy 182 GCCAAGTTCATCAAG 241  
Db 181 GCCAAGTTCATCAAG 240  
Qy 242 ATGAGCGGAGAGTGAAGATCTGCGGAGAGTGTGACCAATGTATGACAGCTGAC 301  
Db 241 ATGAGCGGAGAGTGAAGATCTGCGGAGAGTGTGACCAATGTATGACAGCTGAC 300  
Qy 302 GACGCTTATGAGAACCGGACCGGATGTCATCTTGAAGTATGATCTGAGAGAGAG 361  
Db 301 GACGCTTATGAGAACCGGACCGGATGTCATCTTGAAGTATGATCTGAGAGAGAG 360  
Qy 362 CTCTTCGATTTCTGAGCCAGAGAGAGTCACTGAGTGAAGAGAGAGAGAGAGAG 421  
Db 361 CTCTTCGATTTCTGAGCCAGAGAGAGTCACTGAGTGAAGAGAGAGAGAGAGAG 420  
Qy 422 AAGCAGATCTGATGAGGAGTGAACCTTCAACAAAGAAATTTCTCACTTGAATCTC 481  
Db 421 AAGCAGATCTGATGAGGAGTGAACCTTCAACAAAGAAATTTCTCACTTGAATCTC 480  
Qy 482 AAGCAGAAACATTTATTTTGTGAGCAAGAAATTTCCATTTCCACATCAAGTGAAT 541  
Db 481 AAGCAGAAACATTTATTTTGTGAGCAAGAAATTTCCATTTCCACATCAAGTGAAT 540  
Qy 542 GACTTTGCTGCTGCTCAGAAATGAGATGAGTGAATTTAAGAAATTTTGGAGAG 601  
Db 541 GACTTTGCTGCTGCTCAGAAATGAGATGAGTGAATTTAAGAAATTTTGGAGAG 600  
Qy 602 CCGGAATTTTGTGCTCAGAAATTTGTAATGAGAGAGAGAGAGAGAGAGAGAG 661  
Db 601 CCGGAATTTTGTGCTCAGAAATTTGTAATGAGAGAGAGAGAGAGAGAGAGAG 660  
Qy 662 TGAACATGAGGCTGATACCTACATCTCTTAAAGTGAAGATCCCTTCTTGGAGAG 721  
Db 661 TGAACATGAGGCTGATACCTACATCTCTTAAAGTGAAGATCCCTTCTTGGAGAG 720  
Qy 722 ACGAAGCAGAGAAACATGAGAAATATCAATCAGTGAAGTTCAGCTTGAAGAGAGATTC 781  
Db 721 ACGAAGCAGAGAAACATGAGAAATATCAATCAGTGAAGTTCAGCTTGAAGAGAGATTC 780  
Qy 782 TTCAGCATACGAG 841  
Db 781 TTCAGCATACGAG 840  
Qy 842 CGGAAGCGGCTGACATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901  
Db 841 CGGAAGCGGCTGACATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
Qy 902 CAGCAAGCAGAT 961  
Db 901 CAGCAAGCAGAT 960  
Qy 962 GTCCGAT 1021  
Db 961 GTCCGAT 1020  
Qy 1022 TCCGCTGATGAAG 1081  
Db 1021 TCCGCTGATGAAG 1080  
Qy 1082 ACTGAG 1141  
Db 1081 ACTGAG 1140  
Qy 1142 TAACTGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201

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Db 1141 TAACTGCTTAACTGCTGAGTGGCCGACAGGAGGCTGAGGCTTGGCCGAGGGGCTCCCTTCTG 1200
Qy 1202 TGCAGACTTTTGGACCCAGCTCAGACCAAGCAACCCGGGCGCTCCAGACACTTTTGGCAAG 1261
Db 1201 TGCAGACTTTTGGACCCAGCTCAGACCAAGCAACCCGGGCGCTCCAGACACTTTTGGCAAG 1260
Qy 1262 AGATGGGGCCCAAGAAATTCAGAAAGCTTGCAGGCAACCCAGAGACCTTGGAGACTGTG 1321
Db 1261 AGATGGGGCCCAAGAAATTCAGAAAGCTTGCAGGCAACCCAGAGACCTTGGAGACTGTG 1320
Qy 1322 GCTGTCTTCTGTGAGAGAGCTCCAGCAATTCGCAAGCTTTAATTCCTCAATAAAGAG 1381
Db 1321 GCTGTCTTCTGTGAGAGAGCTCCAGCAATTCGCAAGCTTTAATTCCTCAATAAAGAG 1380
Qy 1382 CTTTCTCTGTGCTGCTGCTCAGAGTCTGGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1441
Db 1381 CTTTCTCTGTGCTGCTGCTCAGAGTCTGGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1440
Qy 1442 TAAAGGACATCTCTCATCATCAAGGGGTGAAGGTCAAGTAAAGGCAAGCTTCTTCAAGGC 1501
Db 1441 TAAAGGACATCTCTCATCATCAAGGGGTGAAGGTCAAGTAAAGGCAAGCTTCTTCAAGGC 1500
Qy 1502 TGAAGGGGTTCAAGAACCACTGCTGCAAAATTAACAAGGCAAGCAAGTCTTCTTCAAGGC 1561
Db 1501 TGAAGGGGTTCAAGAACCACTGCTGCAAAATTAACAAGGCAAGCAAGTCTTCTTCAAGGC 1560
Qy 1562 TGGGAACAGGGGTATTGAGAAAGTGAACCTTGGGTGAGAGGACCAATCCTGTGACCTC 1621
Db 1561 TGGGAACAGGGGTATTGAGAAAGTGAACCTTGGGTGAGAGGACCAATCCTGTGACCTC 1620
Qy 1622 CCAGAACCATGAAAGCCAGAGACCTCAGCTGACCAACACTTCAAGCTTCTTGAAGAGCC 1681
Db 1621 CCAGAACCATGAAAGCCAGAGACCTCAGCTGACCAACACTTCTGAAGAGAGCC 1680
Qy 1682 CATTCGCTGGCCGCGCATGTGTATTTTGTCTATTTTATTAACCTTGTGTTTACTGA 1741
Db 1681 CATTCGCTGGCCGCGCATGTGTATTTTGTCTATTTTATTAACCTTGTGTTTACTGA 1740

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RESULT 5  
us-09-649-163-9895  
Sequence 9895, Application US/09649163

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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine A.
APPLICANT: Leiby, Kevin R.
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Weich, Nadine S.
APPLICANT: McCarthy, Sean A.
APPLICANT: Williamson, Mark
APPLICANT: Richardson, Jennifer
APPLICANT: MacBeth, Kyle J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Villaveal, Jean-Luc M.G.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Siles-Santiago, Inmaculada
APPLICANT: White, David
APPLICANT: Pan, Yang
APPLICANT: Busfield, Samantha J.
APPLICANT: Deeds, James
APPLICANT: Lee, John
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.1164-001
CURRENT APPLICATION NUMBER: US/09/649,163
PRIOR APPLICATION NUMBER: 60/150,608
NUMBER OF SEQ ID NOS: 10535
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9895

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; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-649-163-9895
Query Match 99.2%; Score 1728.8; DB 25; Length 2235;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ACCGGGCGAGCTCAGCTTCCCGGCGATTTGATGTCAGAGCTCAATGAGAGTCCAAAC 61
Db 1 ACCGGGCGAGCTCAGCTTCCCGGCGATTTGATGTCAGAGCTCAATGAGAGTCCAAAC 60
Qy 62 ATGAGCCATTCAAGCAGAGAGGTGAGAGCTTTATGATCATGAGAGAGTCTGGG 121
Db 61 ATGAGCCATTCAAGCAGAGAGGTGAGAGCTTTATGATCATGAGAGAGTCTGGG 120
Qy 122 AGTGGCCAGTTGGCCATCTGTGAAGAGTCCCGGAGAAAGACCGGGGCTTGAATGCA 181
Db 121 AGTGGCCAGTTGGCCATCTGTGAAGAGTCCCGGAGAAAGACCGGGGCTTGAATGCA 180
Qy 182 GCCAAGTTCAATCAAGAGCGGAGAGCCGAGCGGCGGTGTGAGCCGGAGAG 241
Db 181 GCCAAGTTCAATCAAGAGCGGAGAGCCGAGCGGCGGTGTGAGCCGGAGAG 240
Qy 242 ATGAGCGGAGGTGAGCATCTGCGGCAAGTCTGACCAATGTCATCAAGCTGCAC 301
Db 241 ATGAGCGGAGGTGAGCATCTGCGGCAAGTCTGACCAATGTCATCAAGCTGCAC 300
Qy 302 GACGCTTATGAAACCGCACCGAGGTGTCATCTTGAAGTGTGAGAGAG 361
Db 301 GACGCTTATGAAACCGCACCGAGGTGTCATCTTGAAGTGTGAGAGAG 360
Qy 362 CTCTTCATTTCTGCGCCAGAGAGTCACTAGTGAAGAGAGGCCACCACTTCA 421
Db 361 CTCTTCATTTCTGCGCCAGAGAGTCACTAGTGAAGAGAGGCCACCACTTCA 420
Qy 422 AAGCAGATCTGAGTGGGGTGAATCACTTCAACAAAGAAATTTGCTCTTGA 481
Db 421 AAGCAGATCTGAGTGGGGTGAATCACTTCAACAAAGAAATTTGCTCTTGA 480
Qy 482 AAGCAGAAACATTTATTTTGTAGCAAGAAATTTCCATTCACACATCAAGCTGAT 541
Db 481 AAGCAGAAACATTTATTTTGTAGCAAGAAATTTCCATTCACACATCAAGCTGAT 540
Qy 542 GACTTTGTCTGCTCAGAAATTAAGATGAGTGAATTTAAGATTTTGGAGC 601
Db 541 GACTTTGTCTGCTCAGAAATTAAGATGAGTGAATTTAAGATTTTGGAGC 600
Qy 602 CCGGAATTTGTGCTCCGAAATTTGTGAATCAAGAGCCCTGGTCTGAGGCTGACATG 661
Db 601 CCGGAATTTGTGCTCCGAAATTTGTGAATCAAGAGCCCTGGTCTGAGGCTGACATG 660
Qy 662 TGGACATAGGCGTCACTACATCTCTTAAGTGAAGATCCCTTTCTGGAGAC 721
Db 661 TGGACATAGGCGTCACTACATCTCTTAAGTGAAGATCCCTTTCTGGAGAC 720
Qy 722 ACGAAGCAGAAACCTGCAATTAATCAATCAGAGCTTCAAGCTTTGATGAGAAATTC 781
Db 721 ACGAAGCAGAAACCTGCAATTAATCAATCAGAGCTTCAAGCTTTGATGAGAAATTC 780
Qy 782 TTCAGCATAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTAAAGAGAC 841
Db 781 TTCAGCATAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTAAAGAGAC 840
Qy 842 CCGAAACGGCTCAATCCAAAGGCTCTCAGACACCTCTGATATACGCCGTGGAGAAC 901
Db 841 CCGAAACGGCTCAATCCAAAGGCTCTCAGACACCTCTGATATACGCCGTGGAGAAC 900
Qy 902 CAGCAAGCATGTGAGAGAGGAGTGTGTCATCTGAGAACTTCAGAAAGAGAT 961
Db 901 CAGCAAGCATGTGAGAGAGGAGTGTGTCATCTGAGAACTTCAGAAAGAGAT 960

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Qy 962 GTCCGACGCGGTGAGACCTTTCTTCAAGATCGTGTCTGTGACACCTCAACCCGC 1021
|
|
|
Db 961 GTCCGACGCGGTGAGACCTTTCTTCAAGATCGTGTCTGTGACACCTCAACCCGC 1020
|
|
|
Qy 1022 TCGCTGATGAAGAGTGCACCTGAGCGCGGATGAGACCTGAGAACTGTGAGAGTAC 1081
|
|
|
Db 1021 TCGCTGATGAAGAGTGCACCTGAGCGCGGATGAGACCTGAGAACTGTGAGAGTAC 1080
|
|
|
Qy 1082 ACTGAGGAGGACATGCGCAGAGAGAAACCTCCACCCAGGAGAGAGAGACCTCC 1141
|
|
|
Db 1081 ACTGAGGAGGACATGCGCAGAGAGAAACCTCCACCCAGGAGAGAGAGACCTCC 1140
|
|
|
Qy 1142 TAACTGCGCTGACCTGACGTGCGCGCCAGGAGGATTGGGCCCAAGCGGAGCTCCCTTCTG 1201
|
|
|
Db 1141 TAACTGCGCTGACCTGACGTGCGCGCCAGGAGGATTGGGCCCAAGCGGAGCTCCCTTCTG 1200
|
|
|
Qy 1202 TGCGACATTTTGGACCCAGCTCAAGACCAAGACCCGGGCGTCTGAGACATTTTGGAAAG 1261
|
|
|
Db 1201 TGCGACATTTTGGACCCAGCTCAAGACCAAGACCCGGGCGTCTGAGACATTTTGGAAAG 1260
|
|
|
Qy 1262 AGATGGGCCCCAAGAAATTCAGAAAGCTTGCAGGCAAGCAGAGACCTGGGAGCTGTG 1321
|
|
|
Db 1261 AGATGGGCCCCAAGAAATTCAGAAAGCTTGCAGGCAAGCAGAGACCTGGGAGCTGTG 1320
|
|
|
Qy 1322 GCTGTCTTCTGTGAGAGAGGCTCCAGCATTCCTCAAGCTTTAATTCTCAATAAATGG 1381
|
|
|
Db 1321 GCTGTCTTCTGTGAGAGAGGCTCCAGCATTCCTCAAGCTTTAATTCTCAATAAATGG 1380
|
|
|
Qy 1382 CTTTCTCTGTCTGTGACATCTCAAGTCTGGGCTGGAGTGTGACCTTGAAGAAACAATA 1441
|
|
|
Db 1381 CTTTCTCTGTCTGTGACATCTCAAGTCTGGGCTGGAGTGTGACCTTGAAGAAACAATA 1440
|
|
|
Qy 1442 TAAAGGACATCTCATCAACGCGGTGAGAGTCAAGATTAAGGCAAGCTTCTTCAACAGGC 1501
|
|
|
Db 1441 TAAAGGACATCTCATCAACGCGGTGAGAGTCAAGATTAAGGCAAGCTTCTTCAACAGGC 1500
|
|
|
Qy 1502 TGAGGGGGTTCAGAACCAAGCTGTGCAAAATTAACACAGAGAGACAGAGTCTTCCCAT 1561
|
|
|
Db 1501 TGAGGGGGTTCAGAACCAAGCTGTGCAAAATTAACACAGAGAGACAGAGTCTTCCCAT 1560
|
|
|
Qy 1562 TGGGAAACGGGTGATTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCTGTGACCTC 1621
|
|
|
Db 1561 TGGGAAACGGGTGATTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCTGTGACCTC 1620
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|
|
Qy 1622 CCAGAACCATGAAAGCCAGAGCGTCAAGCTCAACCACTCAAGCTTCTGAAAGCAAGC 1681
|
|
|
Db 1621 CCAGAACCATGAAAGCCAGAGCGTCAAGCTCAACCACTCAAGCTTCTGAAAGCAAGC 1680
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|
|
Qy 1682 CATTGCTGCGCGCATGTTGTAATTTTGTCAATTTTAACTTCTGTTTAACTGTA 1741
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|
|
Db 1681 CATTGCTGCGCGCATGTTGTAATTTTGTCAATTTTAACTTCTGTTTAACTGTA 1740
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RESULT 6
US-09-652-917-3775
; Sequence 3775, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652.917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 3775
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-652-917-3775
Query Match 99.2%; Score 1728.8; DB 25; Length 2235;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ACCGCGGAGCTCAAGCTCCCGCGAATTTGATGTTCCAGGCTCAATGAGAGTCCAAAC 61
|
|
|
Db 1 ACCGCGGAGCTCAAGCTCCCGCGAATTTGATGTTCCAGGCTCAATGAGAGTCCAAAC 60
|
|
|
Qy 62 ATGAGACCATTCAGACGACAGAGAGTGAAGACCTTTTATGACATTCGAGAGAGAGCTGGGG 121
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|
|
Db 61 ATGAGACCATTCAGACGACAGAGAGTGAAGACCTTTTATGACATTCGAGAGAGAGCTGGGG 120
|
|
|
Qy 122 AGTGGCCAGTTTGTGCATCGTGAAGAGTCCGGGAGAGACAGAGGCTTGAGTATGCA 181
|
|
|
Db 121 AGTGGCCAGTTTGTGCATCGTGAAGAGTCCGGGAGAGACAGAGGCTTGAGTATGCA 180
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|
|
Qy 182 GCCAAGTTTCATCAAGAACGCGCAGAGCCGGCGAGCCGCGGTGTGAGCCGGGAGAGAG 241
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|
|
Db 181 GCCAAGTTTCATCAAGAACGCGCAGAGCCGGCGAGCCGCGGTGTGAGCCGGGAGAGAG 240
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|
|
Qy 242 ATCGAGCGGAGGTGAGCATCTCGCGGAGGTGCTGCACCAATGTCATACGCTGCAC 301
|
|
|
Db 241 ATCGAGCGGAGGTGAGCATCTCGCGGAGGTGCTGCACCAATGTCATACGCTGCAC 300
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|
|
Qy 302 GACGCTATGAGAACCGCACGAGTGTGACATCCTTGGCTAAGTCTGAGAGAGAG 361
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|
|
Db 301 GACGCTATGAGAACCGCACGAGTGTGACATCCTTGGCTAAGTCTGAGAGAGAG 360
|
|
|
Qy 362 CTTTCTGATTTCTCGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACCAAGCTTCAAT 421
|
|
|
Db 361 CTTTCTGATTTCTCGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACCAAGCTTCAAT 420
|
|
|
Qy 422 AAGCAGATCTCGATGAGGAGTGAATCTTCAACAAAGAAATTTGCTCACTTGTATTC 481
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|
|
Db 421 AAGCAGATCTCGATGAGGAGTGAATCTTCAACAAAGAAATTTGCTCACTTGTATTC 480
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|
|
Qy 482 AAGCAGAAACATTAATGTTGTAGACAAATTTCCATTCACACATCAACATCACTGATT 541
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|
|
Db 481 AAGCAGAAACATTAATGTTGTAGACAAATTTCCATTCACACATCAACATCACTGATT 540
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|
|
Qy 542 GACTTTGCTGTGCTCAAGAAATGAGATGAGTGAATTTAAGAAATATTTTGGAGC 601
|
|
|
Db 541 GACTTTGCTGTGCTCAAGAAATGAGATGAGTGAATTTAAGAAATATTTTGGAGC 600
|
|
|
Qy 602 CCGGAATTTGTTGCTCCAGAAATTTGTAATGAGGCCCTGGGTCTGAGAGCTGACATG 661
|
|
|
Db 601 CCGGAATTTGTTGCTCCAGAAATTTGTAATGAGGCCCTGGGTCTGAGAGCTGACATG 660
|
|
|
Qy 662 TGGAGCATAGGCGTCACTACATCTCTTAAGTGAAGATCCCTTCTTCTGGAGAC 721
|
|
|
Db 661 TGGAGCATAGGCGTCACTACATCTCTTAAGTGAAGATCCCTTCTTCTGGAGAC 720
|
|
|
Qy 722 ACGAAGCAGAAACACTGGGCAATATCAATCAGTGAATTCAGACTTGTATGAGAAATTC 781
|
|
|
Db 721 ACGAAGCAGAAACACTGGGCAATATCAATCAGTGAATTCAGACTTGTATGAGAAATTC 780
|
|
|
Qy 782 TTCAAGCATAGAGCGAGCTGGCCAGAGACTTTAATTCGAAAGCTTCTGTAAAGAGACC 841
|
|
|
Db 781 TTCAAGCATAGAGCGAGCTGGCCAGAGACTTTAATTCGAAAGCTTCTGTAAAGAGACC 840
|
|
|
Qy 842 CGGAAAGGCTCAATTCAGAGAGGCTCTCAGACACCCCTGATCAAGCCGCTGAGCAAC 901
|
|
|
Db 841 CGGAAAGGCTCAATTCAGAGAGGCTCTCAGACACCCCTGATCAAGCCGCTGAGCAAC 900
|
|
|
Qy 902 CAGCAAGCATGTCAGAGCGGAGTCTGTGTCATCTGAGAACTTCAGGAACAGAT 961
|
|
|
Db 901 CAGCAAGCATGTCAGAGCGGAGTCTGTGTCATCTGAGAACTTCAGGAACAGAT 960
|
|
|
Qy 962 GTCCGACGCGGTGAGAGCTTCTTCAAGATCGTGTCTGTGACCAACCTCAACCCGC 1021
|
|
|
Db 961 GTCCGACGCGGTGAGAGCTTCTTCAAGATCGTGTCTGTGACCAACCTCAACCCGC 1020
|
|
|
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Qy	1022	TCGCTGATGAAAGAGTGACCTTGAGCTCGGATGAGACCTTGAGGAACTGTGAGAGTAC	1081
Db	1021	TCGCTGATGAAAGAGTGACCTTGAGGCTGGATGAGACTTGAGAACTGTGAGAGTAC	1080
Qy	1082	ACTGAGAGGACATGGCCAGAGAGAAACCTTCACCCAGAGAGAGCAGACCTCC	1141
Db	1081	ACTGAGAGGACATCCCGAGAGGAAAGCCCTCCACCCAGAGAGAGCAGACCTCC	1140
Qy	1142	TAACTGCGCTGACCTGCACTGAGTGGCCCGCAGAGAGGCTTGGGGCCAGCGGGGCTCCCTCTG	1201
Db	1141	TAACTGCGCTGACCTGCACTGAGTGGCCCGCAGAGAGGCTTGGGGCCAGCGGGGCTCCCTCTG	1200
Qy	1202	TGCGACATTTTGGAGCCGAGCTCAGACACAGCACCCGGGCGTCTTGACACTTTGCAAGAG	1261
Db	1201	TGCGACATTTTGGAGCCGAGCTCAGACACAGCACCCGGGCGTCTTGACACTTTGCAAGAG	1260
Qy	1262	AGATGGGCCCAAGAAATTCAGAAAGCTTTCAGAGCAACCCAGAGAGCCCTGGGAGCTGAG	1321
Db	1261	AGATGGGCCCAAGAAATTCAGAAAGCTTTCAGAGCAACCCAGAGAGCCCTGGGAGCTGAG	1320
Qy	1322	GCTGCTCTCTGAGAGAGGCTCCAGCATTCCCAAAGCTTTAATCTCCATAAATGGG	1381
Db	1321	GCTGCTCTCTGAGAGAGGCTCCAGCATTCCCAAAGCTTTAATCTCCATAAATGGG	1380
Qy	1382	CTTTCCTCTGCTGTCATCTCAGAGTCTGGGGTGGAGATGTGACCTGAGAAACAATA	1441
Db	1381	CTTTCCTCTGCTGTCATCTCAGAGTCTGGGGTGGAGATGTGACCTGAGAAACAATA	1440
Qy	1442	TAAAGGACATCTCTCATCATCACGGGGTGAAGGTCAAGATPAAGCAAGCTTCTTCAAGGC	1501
Db	1441	TAAAGGACATCTCTCATCATCAAGGGGTGAAGGTCAAGCTPAAGCAAGCTTCTTCAAGGC	1500
Qy	1502	TGAGGGGTTTCAGAACCAAGCTGGCCCAAAATTAACACAGAGAGCAGAGTCTGCCCAT	1561
Db	1501	TGAGGGGTTTCAGAACCAAGCTGGCCCAAAATTAACACAGAGAGCAGAGTCTGCCCAT	1560
Qy	1562	TGGGAACAGGGTGAATTGAGAAAGTGAACCTTGGGTGTGAAGGACCAATCTGTGACCTC	1621
Db	1561	TGGGAACAGGGTGAATTGAGAAAGTGAACCTTGGGTGTGAAGGACCAATCTGTGACCTC	1620
Qy	1622	CCAGAACCATGAAAGCCAGAACGTCAAGCTGACCAACCTCGAGACCTTCTGACACACC	1681
Db	1621	CCAGAACCATGAAAGCCAGAACGTCAAGCTGACCAACCTCGAGACCTTCTGACACACC	1680
Qy	1682	CATTGCTGGGCCGCATGTTGTAAATTTTGCTATTTTATTAACCTTCTGCTTAACCTGA	1741
Db	1681	CATTGCTGGGCCGCATGTTGTAAATTTTGCTATTTTATTAACCTTCTGCTTAACCTGA	1740

RESULT 7  
US-09-698-010-12235

GENERAL INFORMATION:  
APPLICANT: Williamson, Mark  
APPLICANT: Shyjan, Andrew W.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

: CURRENT APPLICATION NUMBER: US/09/698,010  
 :  
 : CURRENT FILING DATE: 2000-10-27  
 :  
 : PRIOR APPLICATION NUMBER: 60/162,358  
 :

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12235
LENGTH: 2235
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-010-12235

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Query Match	99.2%;	Score 1728.8;	DB 27;	Length 2235;
Best Local Similarity	99.6%;	Pred. No. 0;		

Matches 1733;	Conservative	0;	Mismatches	7;	Indels	0;	Gaps	0;
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[illegible]

QY 1082 ACTGAGAGGACATCGCAGAGAGGAAAGCCCTCCACCCACGAGAGGAGAGCAGCCTCC 1141  
 Db 1081 ACTGAGAGGAGCATCGCAGAGAGGAAAGCCCTCCACCCACGAGAGGAGAGCAGCCTCC 1140  
 QY 1142 TAACTGCGCTTACCTGCGAGGTGCGCCGAGGAGGTTTGGGCCAGCGGGGCTCCCTTCTG 1201  
 Db 1141 TAACTGCGCTTACCTGCGAGGTGCGCCGAGGAGGTTTGGGCCAGCGGGGCTCCCTTCTG 1200  
 QY 1202 TGCGAGACTTTTGGACCCAGCTCAGACCCAGGAGGCTCTGAGGACTTTTGGAGAG 1261  
 Db 1201 TGCGAGACTTTTGGACCCAGCTCAGACCCAGGAGGCTCTGAGGACTTTTGGAGAG 1260  
 QY 1262 AGATGGGCGCAAGGATTGAGAGAGCTTTGAGGAGGAGAGAGCCCTGGAGCTGTG 1321  
 Db 1261 AGATGGGCGCAAGGATTGAGAGAGCTTTGAGGAGGAGAGAGCCCTGGAGCTGTG 1320  
 QY 1322 GCTGCTTCTGTGAGAGAGGCTCCAGCAATTCGCAAGCTTTAATTCTTCATTAAGTGG 1381  
 Db 1321 GCTGCTTCTGTGAGAGAGGCTCCAGCAATTCGCAAGCTTTAATTCTTCATTAAGTGG 1380  
 QY 1382 CTTCCTCTGCTGCTGCTCAGAGCTCGGGGTGGAGGTGGAGCTTAAGAGAAACAATA 1441  
 Db 1381 CTTCCTCTGCTGCTGCTCAGAGCTCGGGGTGGAGGTGGAGCTTAAGAGAAACAATA 1440  
 QY 1442 TAAAGACATCTCATCATCAAGGGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 1501  
 Db 1441 TAAAGACATCTCATCATCAAGGGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 1500  
 QY 1502 TGAGGGGGTTCAGAACAGAGCTGCGCAAAATTAACACAGAGAGAGAGAGTCTCCCAT 1561  
 Db 1501 TGAGGGGGTTCAGAACAGAGCTGCGCAAAATTAACACAGAGAGAGAGAGTCTCCCAT 1560  
 QY 1562 TGGGAAACAGGGTGAATTGAGAAAGTGAACCTTGGGTGAGAGAGCAATCTGTGACCTC 1621  
 Db 1561 TGGGAAACAGGGTGAATTGAGAAAGTGAACCTTGGGTGAGAGAGCAATCTGTGACCTC 1620  
 QY 1622 CCAGAACCATGGAAGCCAGAGCTGAGGCTGACCAACACTCAGACTTCTGAGAGAGCC 1681  
 Db 1621 CCAGAACCATGGAAGCCAGAGCTGAGGCTGACCAACACTCAGACTTCTGAGAGAGCC 1680  
 QY 1682 CATGCTGGCCCCCGCATGTGTAATTTTGTCTCATTTTAACTTGTGTTAACTGTA 1741  
 Db 1681 CATGCTGGCCCCCGCATGTGTAATTTTGTCTCATTTTAACTTGTGTTAACTGTA 1740

RESULT 8  
 US-09-698-013-6041  
 ; Sequence 6041, Application US/09698013  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gearing, David P.  
 ; APPLICANT: Comrack, Christopher  
 ; APPLICANT: Kingsbury, Gillian A.  
 ; APPLICANT: Holzman, Douglas A.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
 ; FILE REFERENCE: 1600, 2013-001  
 ; CURRENT APPLICATION NUMBER: US/09/698, 013  
 ; CURRENT FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: 60/162,360  
 ; NUMBER OF SEQ ID NOS: 7935  
 ; SOFTWARE: FaastSeq for Windows Version 4.0  
 ; SEQ ID NO 6041  
 ; LENGTH: 2235  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-698-013-6041

Query Match 99.2%; Score 1728.8; DB 27; Length 2235;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACCGCGAGCTCAGCCTCCCGCGAATTGATGTTCCAGGCGCTCAATGAGAGTCCAAAC 61  
 Db 1 ACCGCGAGCTCAGCCTCCCGCGAATTGATGTTCCAGGCGCTCAATGAGAGTCCAAAC 60  
 QY 62 ATGAGGCTTCAAG 121  
 Db 61 ATGAGGCTTCAAG 120  
 QY 122 AGTGGCCAGTTTGGCATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 181  
 Db 121 AGTGGCCAGTTTGGCATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 180  
 QY 182 GCCAAGTTTCATCAAG 241  
 Db 181 GCCAAGTTTCATCAAG 240  
 QY 242 ATCGAGCGGAG 301  
 Db 241 ATCGAGCGGAG 300  
 QY 302 GACGCTATGAGAACCGGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361  
 Db 301 GACGCTATGAGAACCGGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 QY 362 CTCTTCGATTTCTGCGCCAG 421  
 Db 361 CTCTTCGATTTCTGCGCCAG 420  
 QY 422 AAGCAGATCTGAGATGGGGTGAATCACTTCAACAAGAAATTTGCTCACTTTGATTC 481  
 Db 421 AAGCAGATCTGAGATGGGGTGAATCACTTCAACAAGAAATTTGCTCACTTTGATTC 480  
 QY 482 AAGCAGAAACATTAATGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541  
 Db 481 AAGCAGAAACATTAATGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 QY 542 GACTTTGCTGCTGCTCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601  
 Db 541 GACTTTGCTGCTGCTCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 602 CCGAATTTGTTGCTCAAGAAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661  
 Db 601 CCGAATTTGTTGCTCAAGAAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 QY 662 TGGAGCATAGGCGTCAATCACTTCAATCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 721  
 Db 661 TGGAGCATAGGCGTCAATCACTTCAATCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 QY 722 ACGAAGCAGAAACATGAGCAATATATCATCATGATGATGATGATGATGATGATGATGAT 781  
 Db 721 ACGAAGCAGAAACATGAGCAATATATCATCATGATGATGATGATGATGATGATGATGAT 780  
 QY 782 TTGAGCCATAG 841  
 Db 781 TTGAGCCATAG 840  
 QY 842 CGGAAACGCTCAATATCAAG 901  
 Db 841 CGGAAACGCTCAATATCAAG 900  
 QY 902 CAGCAAGCATGAGTGCAGAT 961  
 Db 901 CAGCAAGCATGAGTGCAGAT 960  
 QY 962 GTCCGAGCGGTGAAAGCTTTCTTCAAGATCGTGTCCGTGCAACCACTCAGCCGC 1021  
 Db 961 GTCCGAGCGGTGAAAGCTTTCTTCAAGATCGTGTCCGTGCAACCACTCAGCCGC 1020  
 QY 1022 TCGCTGATGAAG 1081  
 Db 1021 TCGCTGATGAAG 1080  
 QY 1082 ACTGAGAGAGACATCGCAG 1141





Qy	687	TCCTTAAAGGGAGCATCCCTTTCCTGGAGACACAAAGCAGAAAACATGGCCAAATA	746
Db	300	TCAGCTTAAGTGGAGCATCCCTTTCCTGGAGACACAAAGCAGAAAACATGGCCAAATA	359
Qy	747	TCACATCAGTGAATTAGCATTTGATGAGAAATTTCTACGCCATACAGACGAGCTGGCCA	806
Db	360	TCACAGCAGTGAATTAGCATTTGATGAGAAATTTCTACGCCAGACGAGCTGGCCA	419
Qy	807	AGGACTTTATTCGGAAAGCTTCGTGTTAAAGAGCCGGGAAAGGGCTCAATCCAAAGAG	866
Db	420	AGGACTTTATTCGGAAAGCTTCGTGTTAAAGAGCCGGGAAAGGGCTCAATCCAAAGAG	479
Qy	867	CTCTCAGACACCCCTGGATCAGCCGGTGGACAAACAGCAAGCCATGTGTGCACGGGAGT	926
Db	480	CTCTCAGACACCCCTGGATCAGCCGGTGGACAAACAGCAAGCCATGTGTGCCAGGAGAT	539
Qy	927	CTGTGTGCATCTTGGAGAACTTTCAGAGACGATATGTCCGACAGCGGTGGAAAGCTTTCT	986
Db	540	CTGTGTGCATCTTGGAGAACTTTCAGAGACGATATGTCCGACAGCGGTGGAAAGCTTTCT	599
Qy	987	TCACATCAGTGCCTCTGTGCACCACTCACCCGCTCGCTGATGAAAGAGTGCACCTGA	1044
Db	600	TCACATCAGTGCCTCTGTGCACCACTCACCCGCTCGCTGATGAAAGAGTGCACCTGA	659
Qy	1047	GGCCGATGAGAACCTGAGGAACCTGTGAGAGTGCACCTGAGAGAGCATCGCCAGAGGA	1100
Db	660	GGCCGATGAGAACCTGAGGAACCTGTGAGAGTGCACCTGAGAGAGCATCGCCAGAGGA	719
Qy	1107	AAGCCCTCCACCCACGGAGAGAGACAGCACCTCTCTAACTGGGCTGTGACCTGCAAGTGGCCG	1166
Db	720	AAGCCCTCCACCCACGGAGAGAGACAGCACCTCTCTAACTGGGCTGTGACCTGCAAGTGGCCG	779
Qy	1167	CAGAGGAGTGTGGAGCCACAGCGGGGCTCCCTTGTGTGCAGACTTTTGGACCCAGCTCAGC	1224
Db	780	CAGAGGAGTGTGGAGCCACAGCGGGGCTCCCTTGTGTGCAGACTTTTGGACCCAGCTCAGC	839
Qy	1227	ACCAAGCACCCGGGAGCTCTTGAAGCATTTTGCAGAAGATGGGCCCAAGAAATTCAGAGAA	1288
Db	840	ACCAAGCACCCGGGAGCTCTTGAAGCATTTTGCAGAAGATGGGCCCAAGAAATTCAGAGAA	899
Qy	1287	GCTTGCAGGCAAGCAGAGAAACCTGGAGAGTGTGCTGTCTCTCTGTGAGAGAGGCTTCA	1344
Db	900	GCTTGCAGGCAAGCAGAGAAACCTGGAGAGTGTGCTGTCTCTCTGTGAGAGAGGCTTCA	959
Qy	1347	GCATTTCCAAAGCTTTAATTCTCAATAAATGGGCTTTCTCTGTGTGCATCCTCAGA	1400

Qy	1407	GTCTGGGGTGGGAGTGTGGA	CTTAGGAAAA	CAATATTAAGGACATCTCATCATCGGG	1466
Dy	1020	GTCTGGGGTGGGAGTGTGGA	CTTAGGAAAA	CAATATTAAGGACATCTCATCATCGGG	1077
Qy	1467	GTGAGGTCAAGAGTAAGGCA	GCCCTTCTTCA	CAGGCTGAGGGGGTTCAGAACGACCTGGC	1524
Dy	1080	GTGAAGGTCAAGACTTAAGGCA	GCCCTTCTTCA	CAGGCTGAGGGGGTTCAGAACGACCTGGC	1134
Qy	1527	CAAAATTAATACAGAGAGACA	BAGTCCTCCCATTTGGGAA	CAGGGTGATTAGGAAN	1588
Dy	1140	CAAAATTAATACAGAGAGACA	BAGTCCTCCCATTTGGGAA	CAGGGTGATTAGGAAN	1199
Qy	1587	GAACTTGGGTGTGAGGAGCA	CAATCTGTGACCTCCAGAACCATGAGAACGAGACGTC	1646	
Dy	1200	GAACTTGGGTGTGAGGAGCA	CAATCTGTGACCTCCAGAACCATGAGAACGAGACGTC	1255	
Qy	1647	AGGCTGACCAACCTTCAAGC	CTTTGAAGCAGCCATTTGCTGGCCCGGACATGTTGTAT	1700	
Dy	1260	AGGCTGACCAACCTTCAAGC	CTTTGGAAGCAGCCATTTGCTGGCCCGGACATGTTGTAT	1314	

Db 1320 TTGGCTCATTTTATTAATAACTTCTGSGTTTACTGA 1354

RESULT 11  
 US-60-360-207-3361  
 ; Sequence 3361, Application us/60360207  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig  
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
 ; FILE REFERENCE: C0001321  
 ; CURRENT APPLICATION NUMBER: US/60/360,207  
 ; CURRENT FILING DATE: 2002-03-01  
 ; NUMBER OF SEQ ID NOS: 47235  
 ; SEQ ID NO 3361  
 ; LENGTH: 1732  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; US-60-360-207-3361

Query Match 59.3%; Score 1032.4; DB 80; Length 1732;  
 Best Local Similarity 83.8%; Pred. No. 7e-243;  
 Matches 1263; Conservative 0; Mismatches 186; Indels 59; Gaps 6;

QY 8 GCAGCTCAGCCCTCCCGCATTTGATGTTCCAGGCTCATAGAGATCCAAACATGAG 67  
 DB 91 GCAGCCAGCTTTCCCGCATTTGATGTTCCAGGCTCATAGAGATCCAAACATGAG 150  
 QY 68 CCATTCAGCAGCAGAGAGTGAAGACTTTTATGATTCGAGAGAGAGTGGGAGTGGC 127  
 DB 151 ACCTTCAGCAGCAGAGAGTGAAGACTTTTATGATTCGAGAGAGAGTGGGAGTGGC 210  
 QY 128 CAGTTTCCATTCGTGAAGAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187  
 DB 211 CAGTTTCCATTCGTGAAGAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270  
 QY 188 TTCTCAAGAGAGCAG 247  
 DB 271 TTCTCAAG 330  
 QY 248 CGGAGAGTGAAGATCTTCGCGCAGAGTGTGACCAATGTCATCGCTGACAGAGTC 307  
 DB 331 CGGAGAGTGAAGATCTTCGCGCAGAGTGTGACCAATGTCATCGCTGACAGAGTC 390  
 QY 308 TATAGAGAGCAGCAGAGAGTGTGACATCTTGAGCTAGTGTGTGAGAGAGAGCTTTC 367  
 DB 391 TATAGAGAGCAGCAGAGAGTGTGACATCTTGAGCTAGTGTGTGAGAGAGAGCTTTC 450  
 QY 368 GATTTCCTGGCCAGAGAGAGTCACTGAGTGAAGAGAGAGAGAGAGAGAGAGAG 427  
 DB 451 GATTTCCTGGCCAGAGAGAGTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 510  
 QY 428 ATCTCGAGTGGGGTGAATCTTACCTTCACACAAAGAAATTTGCTCACTTGAATCCAGCCA 487  
 DB 511 ATCTCGAGTGGGGTGAATCTTACCTTCACACAAAGAAATTTGCTCACTTGAATCCAGCCA 570  
 QY 488 GAAACATTATGTTGTTAGACAAAGATATTCCTCATTCACATCAAGCTGATTTGATTT 547  
 DB 571 GAAACATTATGTTGTTAGACAAAGATATTCCTCATTCACATCAAGCTGATTTGATTT 630  
 QY 548 GGTCTGGCTCAGAAATGAAATGAGAGTGAATTTAAGATTTTGGAGCCCGGAA 607  
 DB 631 GGTCTGGCTCAGAAATGAAATGAGAGTGAATTTAAGATTTTGGAGCCCGGAA 690  
 QY 608 TTTGTTGCTCCAGAAATTTGAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667  
 DB 691 TTTGTTGCTCCAGAAATTTGAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 746  
 QY 668 ATAGGGCTCATCACTTACCTTTAAGTGAAGATCCCTTCTCTGGAGAGACAGAG 727  
 DB 747 -----TCTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783  
 QY 728 CAGAGAAACCTGGCAATATCATCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 787  
 DB 784 CAGAGAAACCTGGCAATATCATCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 843  
 QY 788 CATACGAGCAGCTGGCCAAAGACTTTATTCGAGAGCTTCTGTTAAAGAGCCCGGAA 847

DB 844 CAGACACGAGAGCTGGCCAAAGACTTCAATTCGGAAGCTTCTTGAAAGAGACCCGAAA 903  
 QY 848 CGGCTCACATTCAGAGAGCTTCTGACACACCCCTGATTCACCGCGGAGCAACACAGAA 907  
 DB 904 CGGCTTACATTCAGAGAGCTTCTGACATCCCTGATTCACCGCGGAGCAACACAGAA 963  
 QY 908 GGCATGTCGCAACCGGAGTCTGTGTCAATCTGAGAGAACTTCAGAGACAGATATGTCGC 967  
 DB 964 GGTATGTACGAGAGAGTCCGTGTCACTGAGAGATTTAAGAGACATATATGTCGC 1023  
 QY 968 AGCGGTGAGAGCTTCTTCAGCATGTCCTGTCGCAACCACTTACCCGCTCGCTG 1027  
 DB 1024 AGCGGTGAGAGCTTCTTCAGCATGTCCTGTCGCAACCACTTACCCGCTCGCTG 1083  
 QY 1028 ATGAGAGAGTCACTTGAAGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087  
 DB 1084 ATGAGAGAGTCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143  
 QY 1088 GAGACATGCGCAG 1147  
 DB 1144 GAGACATGCGCAG 1203  
 QY 1148 GCTTGAACCTGAGTGGCCCGCAGAGAGTGTGGAGCCAGCGGGGCTCCCTGTGACAG 1207  
 DB 1204 GCTTGAACCTGAGTGGCCCGCAGAGAGTGTGGAGCCAGCGGGGCTCCCTGTGACAG 1260  
 QY 1208 CTTTGGAGCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259  
 DB 1261 CTTTGGAGCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
 QY 1260 AGAGATGGGCGCAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319  
 DB 1321 AGAGATGGGCGCAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1368  
 QY 1320 TGGCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379  
 DB 1369 TGGCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1428  
 QY 1380 GGTCTTCTCTGTGTCATCTTCAGAGTGTGGGTGGAGTGTGAGACTTAAGAAACAA 1439  
 DB 1429 GGTCTTCTCTGTGTCATCTTCAGAGTGTGGGTGGAGTGTGAGACTTAAGAAACAA 1487  
 QY 1440 TATTAAG 1491  
 DB 1488 TCTCAAGAGATCTTTTATTTTAAACAGAGTTAAAGTGAATTAAGAGAGCTTT 1547  
 QY 1492 CTTACAG 1499  
 DB 1548 CTTACAG 1555

RESULT 12  
 US-09-649-163-7647  
 ; Sequence 7647, Application US/09649163  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holtzman, Douglas A.  
 ; APPLICANT: Galvin, Katherine A.  
 ; APPLICANT: Leiby, Kevin R.  
 ; APPLICANT: Kingsbury, Gillian A.  
 ; APPLICANT: Welch, Nadine S.  
 ; APPLICANT: McCarthy, Sean A.  
 ; APPLICANT: Williamson, Mark  
 ; APPLICANT: Richardson, Jennifer  
 ; APPLICANT: Macbeth, Kyle J.  
 ; APPLICANT: Frazer, Christopher C.  
 ; APPLICANT: Villevall, Jean-luc M.G.  
 ; APPLICANT: Goodheart, Andrew D.J.  
 ; APPLICANT: Siles-Santiago, Inmaculada  
 ; APPLICANT: White, David  
 ; APPLICANT: Pan, Yang  
 ; APPLICANT: Busfield, Samantha J.  
 ; APPLICANT: Deede, James







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Db 1260 CAGGTGACCAACACCTCAGACCTTCTGAAAGCAGCCCATCTGCGCCGCACTGTTGAA 1319
Qy 1706 TTTGCTCATTTTATTAATACTTCTGTTTACCTGA 1741
Db 1320 TTTGCTCATTTTATTAATACTTCTGTTTACCTGA 1355

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RESULT 15

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US-09-652-917-2793
; Sequence 2793, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyam, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600,1170-001
; CURRENT APPLICATION NUMBER: US/09/652,917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastrSeq for Windows Version 4.0
; SEQ ID NO 2793
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-917-2793

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Query March 58.5%; Score 1019.2; DB 25; Length 1512;

Best Local Similarity 99.1%; Pred. No. 1.2e-239; Matches 8; Indels 2; Gaps 2;

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Qy 687 TCCTCTTAAGTGAAGCATCCCTTCTCTGGAGACACGAAGAGAAACATCGGCAATA 746
Db 301 TCAGCTTAAGTGAAGCATCCCTTCTCTGGAGACACGAAGAGAAACATCGGCAATA 360
Qy 747 TCACATCAGTGAAGTACGACTTTGATGAGAAATTTTCAGCCATACGAGCGAGTGGCA 806
Db 361 TCACAGCAGTGAAGTACGACTTTGATGAGAAATTTTCAGCCATACGAGCGAGTGGCA 420
Qy 807 AGGACTTATTTCGGAAGCTTCTGTTAAAGAACCCGGAAGCGCTCAATCCAGAG 866
Db 421 AGGACTTATTTCGGAAGCTTCTGTTAAAGAACCCGGAAGCGG-TCACAATCCAGAG 479
Qy 867 CTCTCAGACACCCCTGATACGCGCGGTGGAACAACGAGCCATGGTG--CGACGGAG 925
Db 480 CTCTCAGACACCCCTGATACGCGCGGTGGAACAACGAGCCATGGTGCGCGAG 539
Qy 926 TCTGTGTCAACTTGAGAACTTCAGAAAGCATATGTCGCGAGCGGTGGAAGCTTTCC 985
Db 540 TCTGTGTCAACTTGAGAACTTCAGAAAGCATATGTCGCGAGCGGTGGAAGCTTTCC 599
Qy 986 TTCAGCATGTGTCTCTGTGCAACCACTCACCGCTGCTGATGAAGAAGTGCACCTG 1045
Db 600 TTCAGCATGTGTCTCTGTGCAACCACTCACCGCTGCTGATGAAGAAGTGCACCTG 659
Qy 1046 AGGCGGATGAGGACCTGAGGAAGTGAAGTGAACAAGAGAGAGACATGGCCAGAG 1105
Db 660 AGGCGGATGAGGACCTGAGGAAGTGAAGTGAACAAGAGAGACATGGCCAGAG 719
Qy 1106 AAAGCCCTCCACCCAGAGAGAGAGAGACACTTCTAACTGGCTGACCTGAGTGGCC 1165
Db 720 AAAGCCCTCCACCCAGAGAGAGAGAGACACTTCTAACTGGCTGACCTGAGTGGCC 779
Qy 1166 GCCAGGAGGTTTGGGCCAGGCGGGCTCTCTTCTGTGCAACTTTTGAACCACTCAG 1225
Db 780 GCCAGGAGGTTTGGGCCAGGCGGGCTCTCTTCTGTGCAACTTTTGAACCACTCAG 839

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Qy 1226 CACGACACCCGGGCGTCTGAGCACTTTGCAAGAGATGGGCCCAAGGAATTGAGAG 1285
Db 840 CACGACACCCGGGCGTCTGAGCACTTTGCAAGAGATGGGCCCAAGGAATTGAGAG 899
Qy 1286 AGCTTGAGGAGGACGAGAGACCTTGGAGCTGTGCTTCTGTGAGAGAGGCTCC 1345
Db 900 AGCTTGAGGAGGACGAGAGACCTTGGAGCTGTGCTTCTGTGAGAGAGGCTCC 959
Qy 1346 AGCATTTCCAAAGCTTAATTTCTCATTAATAATGGGCTTCTCTGTGTCATCTCAG 1405
Db 960 AGCATTTCCAAAGCTTAATTTCTCATTAATAATGGGCTTCTCTGTGTCATCTCAG 1019
Qy 1406 AGCTGGGGTGGAGTGTGACTTAGAAGAAACAATATAAGAGACATCTCATCATCAGG 1465
Db 1020 AGCTGGGGTGGAGTGTGACTTAGAAGAAACAATATAAGAGACATCTCATCATCAGG 1079
Qy 1466 GGTGAAGGTCAAGTGAAGGACGCTTTCTTCAAGGCTGAGGGGTTTCAAAACAGCTTG 1525
Db 1080 GGTGAAGGTCAAGTGAAGGACGCTTTCTTCAAGGCTGAGGGGTTTCAAAACAGCTTG 1139
Qy 1526 CCAAAAATTACACGAGAGACAGAGTCTCCCATTTGGGAAACAGGCTGATTGAGGAAG 1585
Db 1140 CCAAAAATTACACGAGAGACAGAGTCTCCCATTTGGGAAACAGGCTGATTGAGGAAG 1199
Qy 1586 TGAACCTTGGGTGAGGAGCAATCTGTGACCTCCAGAACATGGAAGCCAGAGAGT 1645
Db 1200 TGAACCTTGGGTGAGGAGCAATCTGTGACCTCCAGAACATGGAAGCCAGAGAGT 1259
Qy 1646 CAGGTGACCAACACTGACACTTCTGAGACAGCCATTGCGCCCGGCAATGTTGTA 1705
Db 1260 CAGGTGACCAACACTGACACTTCTGAGACAGCCATTGCGCCCGGCAATGTTGTA 1319
Qy 1706 TTTGCTCATTTTATTAATACTTCTGTTTACCTGA 1741
Db 1320 TTTGCTCATTTTATTAATACTTCTGTTTACCTGA 1355

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Search completed: Apr-11 4, 2003, 22:30:05  
Job time : 5391.24 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1727.4	59.2	2085	9	US-60-443-566-647	Sequence 647, App
2	1199.8	68.9	1442	6	US-09-724-676-34736	Sequence 34736, App
3	1159.8	68.9	1442	6	US-09-724-676A-34736	Sequence 34736, App
4	1032.4	59.3	1732	8	US-10-144-771-3361	Sequence 3361, App
5	534	30.7	601	5	US-09-947-807-15328	Sequence 15328, App
6	517.2	29.7	2157	5	US-09-949-016-1966	Sequence 1966, App
7	517.2	29.7	2201	9	US-60-443-566-667	Sequence 667, App
8	515.6	29.6	2105	5	US-09-949-016-195	Sequence 195, App
9	515.6	29.6	2132	1	PCT-US02-31357-118	Sequence 118, App
10	515.6	29.6	2132	8	US-10-262-445-118	Sequence 118, App
11	515.4	29.6	2570	6	US-09-724-676-20895	Sequence 20895, App
12	515.4	29.6	2570	6	US-09-724-676A-20895	Sequence 20895, App
13	514.6	29.5	979	6	US-09-724-676-20893	Sequence 20893, App
14	514.6	29.5	979	6	US-09-724-676A-20893	Sequence 20893, App
15	513.8	29.5	1410	8	US-10-144-771-9285	Sequence 9285, App
16	512.4	29.4	5525	8	US-10-144-771-9285	Sequence 9285, App
17	498.4	28.7	1514	1	PCT-US03-03482-3594	Sequence 3594, App
18	498.4	28.7	1514	1	PCT-US03-03194-3489	Sequence 3489, App
19	499.4	28.7	1514	8	US-10-338-044-2139	Sequence 2139, App
20	498.4	28.7	1514	9	US-60-443-566-3489	Sequence 3489, App
21	495.4	28.4	6074	9	US-60-443-566-1691	Sequence 1691, App
22	494.6	28.4	5910	1	PCT-US03-02484-37	Sequence 37, App
23	494.6	28.4	5910	6	US-09-949-002-51	Sequence 51, App
24	494.6	28.4	5910	8	US-10-133-937-12	Sequence 12, App

25	494.6	28.4	5910	8	US-10-303-588-4	Sequence 4, Appl
26	494.6	28.4	5910	8	US-10-159-563-12	Sequence 12, Appl
27	494.6	28.4	5910	8	US-10-347-887-1105	Sequence 1105, Appl
28	494.6	28.4	5910	8	US-10-342-119-19	Sequence 19, Appl
29	490.6	28.2	609	8	US-10-266-111-5686	Sequence 2686, Appl
30	466.8	26.8	5503	6	US-09-949-002-200	Sequence 200, Appl
31	416.8	23.9	601	5	US-09-947-907-15359	Sequence 15359, Appl
32	342.2	19.6	563	6	US-09-533-315B-17944	Sequence 17944, Appl
33	278.8	16.0	1195	1	PCT-UM03-01096-36	Sequence 36, Appl
34	257.8	14.8	520	6	US-09-533-315B-17939	Sequence 17939, Appl
35	247.6	14.0	1526	5	US-09-949-016-11937	Sequence 11937, Appl
36	244.6	14.0	16631	5	US-09-914-016-13708	Sequence 13708, Appl
37	226	13.0	229	6	US-09-911-293-34583	Sequence 34583, Appl
38	224.8	12.9	467	6	US-09-533-315B-17937	Sequence 17937, Appl
39	215.6	12.4	466	8	US-10-310-673-1633	Sequence 1632, Appl
40	215	12.3	326	6	US-09-533-315B-23938	Sequence 23938, Appl
41	207.2	11.9	312	6	US-09-533-315B-23911	Sequence 23911, Appl
42	203	11.7	5926	8	US-10-240-425-1440	Sequence 1440, Appl
43	202.6	11.6	7694	9	US-60-445-135-8838	Sequence 2838, Appl
44	201.4	11.6	1847	5	US-09-949-016-5449	Sequence 5449, Appl
45	201.4	11.6	3164	1	PCT-US02-24567-25	Sequence 25, Appl

## ALIGNMENTS

```

RESULT 1
US-60-443-566-647
: Sequence 647, Application US/60443566
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001447
: CURRENT APPLICATION NUMBER: US/60/443,566
: CURRENT FILING DATE: 2003-01-30
: NUMBER OF SEQ. ID NOS: 25102
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 647
: LENGTH: 2085
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-443-566-647

```

Query Match 99.2%; Score 1727.4; DB 9; Length 2085;

Matches 1728; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy	1	GACCGCGGACACTAGACCTCCCGCGGAAFTGATATGTCGAGGCTCAATGAGAGACTCCAA	60
Db	8	GACCGCGGACACTAGACCTCCCGCGGATTTGATATGTCGAGGCTCAATGAGAGACTCCAA	67
Oy	61	CATGAGGCAATTCAGACGACGAGAGTGAGAGACTTTTATACATCGAGAGAGACTGG	120
Db	68	CATGAGGCAATTCAGACGACGAGAGTGAGAGACTTTTATACATCGAGAGAGACTGG	122
Oy	121	GAGTGGCCAGTTTGCCTCATCGTGAAGAAATGTCGGGAGAGAGACGGGGCTTGAATGC	180
Db	128	GAGTGGCCAGTTTGCCTCATCGTGAAGAAATGTCGGGAGAGAGACGGGGCTTGAATGC	187
Oy	181	AGCCAAAGTTTCATCAAGAAACGGCGACAGAGCCGGGCGAGCCGCGGTGTGAGCCGGAGAG	244
Db	188	AGCCAAAGTTTCATCAAGAAACGGCGACAGAGCCGGGCGAGCCGCGGTGTGAGCCGGAGAG	247
Oy	241	GATCGAGGGGAGGTGAGACATCTCTGCGGCAAGTGTCTGACACCAAAATGTTCATCAGCTGCA	300
Db	248	GATCGAGGGGAGGTGAGACATCTCTGCGGCAAGTGTCTGACACCAAAATGTTCATCAGCTGCA	307
Oy	301	CGACGTCATATGAAACCGGACCGACCGATGAGTGCATATCTTACGTTAGTGTGAGAGAGA	360
Db	308	CGACGTCATATGAAACCGGACCGACCGATGAGTGTCTATCTTGAAGTTAGTGTGAGAGAGA	366

QY 361 GCTCTGATTTTCCGCGCCAGAGAGTCACTGATGAGAGAGGCCACACAGCTTTCAT 420  
 Db 368 GCTCTGATTTTCTGCGCCAGAGAGTCACTGATGAGAGAGGCCACACAGCTTTCAT 427  
 QY 421 TAAGCAGATCCCTGATGAGAGTGAATCTACCTTTCACAAAGAAAATTGCTCATTTGATCT 480  
 Db 428 TAAGCAGATCCCTGATGAGAGTGAATCTACCTTTCACAAAGAAAATTGCTCATTTGATCT 487  
 QY 481 CAAGCCAGAAAACATTAATGTTGTTAGACAGAAATTTCCCATTCACACATCAAGTCTAT 540  
 Db 488 CAAGCCAGAAAACATTAATGTTGTTAGACAGAAATTTCCCATTCACACATCAAGTCTAT 547  
 QY 541 TGACTTTGGTCTGCTCAAGAAATGAAAGATGAGTTGAATTTAAATTTTGGGAC 600  
 Db 548 TGACTTTGGTCTGCTCAAGAAATGAAAGATGAGTTGAATTTAAATTTTGGGAC 607  
 QY 601 GCGGGAATTTGTTGCTCCAGAAATTTGTAACTACAGAGCCCGGGGTCTGAGAGCTGACAT 660  
 Db 608 GCGGGAATTTGTTGCTCCAGAAATTTGTAACTACAGAGCCCGGGGTCTGAGAGCTGACAT 667  
 QY 661 GTGAGACATAGGCGTATACCTACCTTCTTAAGTGGAGCATCCCTTTCCTGGAGA 720  
 Db 668 GTGAGACATAGGCGTATACCTACCTTCTTAAGTGGAGCATCCCTTTCCTGGAGA 727  
 QY 721 CACGAGCAGAGAAACACTGGCAAAATTCATCAGTGAATTCAGCTTTGATGAGAAAT 780  
 Db 728 CACGAGCAGAGAAACACTGGCAAAATTCATCAGTGAATTCAGCTTTGATGAGAAAT 787  
 QY 781 CTTGACACCTACAGAGAGCTGGCCAGAGCTTATTCGAAAGCTTCTGGTAAAGAGAC 840  
 Db 788 CTTGACACCTACAGAGAGCTGGCCAGAGCTTATTCGAAAGCTTCTGGTAAAGAGAC 847  
 QY 841 CCGGAAACGGCTCAACATCCAGAGGCTCTCAGACACCCCTGGATCAGCCGCTGAGCA 900  
 Db 848 YCCGAAACGGCTCAACATCCAGAGGCTCTCAGACACCCCTGGATCAGCCGCTGAGCA 907  
 QY 901 CCAGCAAGCCATGCTGCGACGAGAGTCTGTGTCATCTGGAACCTTCAGAGAGCAGTA 960  
 Db 908 CCAGCAAGCCATGCTGCGACGAGAGTCTGTGTCATCTGGAACCTTCAGAGAGCAGTA 967  
 QY 961 TGTCCGAGGCGGTGAGAGCTTCTCTCAGACATCTGTCTCTGTGCAACCACTCAACCG 1020  
 Db 968 TGTCCGAGGCGGTGAGAGCTTCTCTCAGACATCTGTCTCTGTGCAACCACTCAACCG 1027  
 QY 1021 CTGCTGATGAGAAAGGTGCACTTGAGCCGATGAGAACCTTGAGAACTGTGAGAGTA 1080  
 Db 1028 CTGCTGATGAGAAAGGTGCACTTGAGCCGATGAGAACCTTGAGAACTGTGAGAGTA 1087  
 QY 1081 CACTGAGAGAGACATCCCGCAGAGAGAAAGCCCTCCACCCAGAGAGAGCAGACCTTC 1140  
 Db 1088 CACTGAGAGAGACATCCCGCAGAGAGAAAGCCCTCCACCCAGAGAGAGCAGACCTTC 1147  
 QY 1141 CTAACCTGCTGACCTGAGTGGCCGCGCAGAGAGTTTGGGCCCCAGCGGGCTTCCCTTCT 1200  
 Db 1148 CTAACCTGCTGACCTGAGTGGCCGCGCGCAGAGAGTTTGGGCCCCAGCGGGCTTCCCTTCT 1207  
 QY 1201 GTGCAGACTTTTGGACCCAGCTCAGACACAGACCCCGGGGCTCTTGAGCACTTTGCAAGA 1260  
 Db 1208 GTGCAGACTTTTGGACCCAGCTCAGACACAGACCCCGGGGCTCTTGAGCACTTTGCAAGA 1267  
 QY 1261 GAGATGGGCCCCAAGAAATTCAAGAGCTTGCAGAGCAAGCCAGAGACCTTGAGAGTGT 1320  
 Db 1268 GAGATGGGCCCCAAGAAATTCAAGAGCTTGCAGAGCAAGCCAGAGACCTTGAGAGTGT 1327  
 QY 1321 GGCTGTCTTGTGTGAGAGGCTCCAGACATTCCTCAAGCTCTTAATTTCTCATTAATTTG 1380  
 Db 1328 GGCTGTCTTGTGTGAGAGGCTCCAGACATTCCTCAAGCTCTTAATTTCTCATTAATTTG 1387  
 QY 1381 GCTTTCTCTCTCTGCTGCAATCTCAGAGTCTGGGGGTGGAGTGTGAGACTTGAAGAAACAT 1440  
 Db 1388 GCTTTCTCTCTCTGCTGCAATCTCAGAGTCTGGGGGTGGAGTGTGAGACTTGAAGAAACAT 1447  
 QY 1441 ATAAAGACATCTCATCAACGAGGAGTGAAGTCAAGTAAGGACGCTTCTTCAACGG 1500

Db 1448 ATAAAGACATCTCATCAACGAGGAGTGAAGTCAAGCTAAGCAGCCTTCTTCAACGG 1507  
 QY 1501 CTGAGAGGGTTCAGAAACGACCTTGCCCAAAATTCACACAGAGAGACAGAGTCCCTCCCA 1560  
 Db 1508 CTGAGAGGGTTCAGAAACGACCTTGCCCAAAATTCACACAGAGAGACAGAGTCCCTCCCA 1567  
 QY 1561 TTGGGAACAGGGTGAATTTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCCTGTGACCT 1620  
 Db 1568 TTGGGAACAGGGTGAATTTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCCTGTGACCT 1627  
 QY 1621 CCAGAACCATGAGAACCCAGAGCTGAGCTGACCAACCTTCAGACCTTCTGAAAGCAGC 1680  
 Db 1628 CCAGAACCATGAGAACCCAGAGCTGAGCTGACCAACCTTCAGACCTTCTGAAAGCAGC 1687  
 QY 1681 CCAATGCTGCGCCCATGTTGTAATTTTGCATTTTATTAATTTGCTGTTTACCTG 1740  
 Db 1688 CCAATGCTGCGCCCATGTTGTAATTTTGCATTTTATTAATTTGCTGTTTACCTG 1747  
 QY 1741 A 1741  
 Db 1748 A 1748

RESULT 2  
 US-09-724-676-34736/c  
 ; Sequence 34736, Application US/09724676  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Compugen LTD  
 ; TITLE OF INVENTION: Variants of alternative splicing  
 ; FILE REFERENCE: 129181.4 Compugen  
 ; CURRENT APPLICATION NUMBER: US/09/724,676  
 ; CURRENT FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 97222  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 34736  
 ; LENGTH: 1442  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-724-676-34736

Query Match 68.9%; Score 1199.8; DB 6; Length 1442;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-296;  
 Matches 1201; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCGGCGACCTGAGCTCCCGCCGATTTGATTTTCAGGCTTCAATGAGAGTCCAAA 60  
 Db 1435 GACCGGCGACCTGAGCTCCCGCCGATTTGATTTTCAGGCTTCAATGAGAGTCCAAA 1376  
 QY 61 CATGAGCCATTCAAGCAGAGAGTGTGAGACTTTTAATGACATCGGAGAGAGCTGGG 120  
 Db 1375 CATGAGCCATTCAAGCAGAGAGTGTGAGACTTTTAATGACATCGGAGAGAGCTGGG 1316  
 QY 121 GAGTGGCCAGTTTGCATCTGTAAGAAAGTGCAGGAGAGAGACGCGGCTTGAATGC 180  
 Db 1315 GAGTGGCCAGTTTGCATCTGTAAGAAAGTGCAGGAGAGAGACGCGGCTTGAATGC 1256  
 QY 181 AGCCAAATTCAAGAAAGCGCAGAGCCGCGCAGAGCCGCGCGGTGTGAGCTCCGGAAGA 240  
 Db 1255 AGCCAAATTCAAGAAAGCGCAGAGCCGCGCGCAGAGCCGCGCGGTGTGAGCTCCGGAAGA 1196  
 QY 241 GATCGAGCGGAGTGTGAGATCTGCGGAGGTGTGACACCAATGTCAATCAGCTGCA 300  
 Db 1195 GATCGAGCGGAGTGTGAGATCTGCGGAGGTGTGACACCAATGTCAATCAGCTGCA 1136  
 QY 301 CGACGTCTATGAGAAACCGCAGCGAGGTGTGACATCTTGAAGTGTGTGAGAGAGA 360  
 Db 1135 CGACGTCTATGAGAAACCGCAGCGAGGTGTGACATCTTGAAGTGTGTGAGAGAGA 1076  
 QY 361 GCTCTTCGATTTCTTGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACAGCTTCAT 420  
 Db 1075 GCTCTTCGATTTCTTGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACAGCTTCAT 1016

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Qy 421 TAAGAGATCTGGATGGGTGAACCTACCTTCAACAAGAAATTTGCTCACTTGTATCT 480
Db 1015 TAAACAGATCTGGATGGGTGAACCTACCTTCAACAAGAAATTTGCTCACTTGTATCT 956
Qy 481 CAAGCCAGAAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTAT 540
Db 955 CAAGCCAGAAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTAT 896
Qy 541 TGACTTTGCTGGCTCAAGAAATGAAGATGAGATTGAATTTAAATTTTGGAGC 600
Db 895 TGACTTTGCTGGCTCAAGAAATGAAGATGAGATTGAATTTAAATTTTGGAGC 836
Qy 601 GCCGGAATTTGCTGCTCAAGAAATTTGAACCTAGACGCCCTGGGCTGGAAGCTGACAT 660
Db 835 GCCGGAATTTGCTGCTCAAGAAATTTGAACCTAGACGCCCTGGGCTGGAAGCTGACAT 776
Qy 661 GTGAGCATAGGCGTCACTACCTTACATCTCTTAAGTGGAGATTCCTTTCTGGAGGA 720
Db 775 GTGAGCATAGGCGTCACTACCTTACATCTCTTAAGTGGAGATTCCTTTCTGGAGGA 716
Qy 721 CACGAAGCAGAAAACATGGGAAATATACATCAGTGAATTACGACTTTGAAGAATTT 780
Db 715 CACGAAGCAGAAAACATGGGAAATATACATCAGTGAATTACGACTTTGAAGAATTT 656
Qy 781 CTTGAGCCATACGAGCGAGCTGGCCAGAGACTTTATTGGAAGCTTCTGTTAAAGAGAC 840
Db 655 CTTGAGCCATACGAGCGAGCTGGCCAGAGACTTTATTGGAAGCTTCTGTTAAAGAGAC 596
Qy 841 CCGGAAACGGCTCAACATCCAAAGAGCTCTAGACACCCCTGGATCAGCCGGTGGACAA 900
Db 595 CCGGAAACGGCTCAACATCCAAAGAGCTCTAGACACCCCTGGATCAGCCGGTGGACAA 536
Qy 901 CCAGCAAGCCATGGTGGACGAGAGCTGTGTGTAATTTGAGAGAACTTCAGAGAGCACTA 960
Db 535 CCAGCAAGCCATGGTGGACGAGAGCTGTGTGTAATTTGAGAGAACTTCAGAGAGCACTA 476
Qy 961 TGTCCGAGGCGGTGGAAGCTTTCTTCAGCATGCTGTCTCTGTGCAACAACCTCACCCG 1020
Db 475 TGTCCGAGGCGGTGGAAGCTTTCTTCAGCATGCTGTCTCTGTGCAACAACCTCACCCG 416
Qy 1021 CTCGCTGATGAAGAGGTGACCTGAGGCGGATGAGAGACCTGAGAGAACTGTAGAGTGA 1080
Db 415 CTCGCTGATGAAGAGGTGACCTGAGGCGGATGAGAGACCTGAGAGAACTGTAGAGTGA 356
Qy 1081 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCACCCAGAGAGAGAGACAGACCTC 1140
Db 355 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCACCCAGAGAGAGAGACAGACCTC 296
Qy 1141 CTAACTGGCTGACCTGACGTGCGCCAGAGAGAGTTTGGGCCCGAGCGGGCTCCCTTCT 1200
Db 295 CTAACTGGCTGACCTGACGTGCGCCAGAGAGAGTTTGGGCCCGAGCGGGCTCCCTTCT 236
Qy 1201 GTGCAGA 1207
Db 235 GTGCAGA 229

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## RESULT 3

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US-09-724-676A-34736/c
; Sequence 34736, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34736
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-34736

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Query Match 68.9%; Score 1199.8; DB 6; Length 1442;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-296;  
 Matches 1201; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 GACCGGCGACCTCAGCCTCCCGCATTTGATGTTCCAGGCTTCATAGAGAGTCCAA 60
Db 1435 GACCGGCGACCTCAGCCTCCCGCATTTGATGTTCCAGGCTTCATAGAGAGTCCAA 1376
Qy 61 CATGAGCCATTCAGAGCAGAGAGTGGAGACTTTTATGACATCCGAGAGAGCTGGG 120
Db 1375 CATGAGCCATTCAGAGCAGAGAGTGGAGACTTTTATGACATCCGAGAGAGCTGGG 1316
Qy 121 GAGTGGCCAGTTTCCATTCGTAAGAAAGTGGCGGAGAGAGCAGGGCTTGAATGTC 180
Db 1315 GAGTGGCCAGTTTCCATTCGTAAGAAAGTGGCGGAGAGAGCAGGGCTTGAATGTC 1256
Qy 181 AGCCAACTTCATCAAGAGCGGAGAGCGGCGAGCGGCGGTGTGAGCCGGAGGA 240
Db 1255 AGCCAACTTCATCAAGAGCGGAGAGCGGCGAGCGGCGGTGTGAGCCGGAGGA 1196
Qy 241 GATGAGCGGAGAGTGAAGCATCTCGCGAGAGTGTGCAACCAATGTATCAAGCTGCA 300
Db 1195 GATGAGCGGAGAGTGAAGCATCTCGCGAGAGTGTGCAACCAATGTATCAAGCTGCA 1136
Qy 301 CGAGCTATATGAGAACCGACCGACGTTGTCATCTCCTGAGCTAGTGTGAGAGGA 360
Db 1135 CGAGCTATATGAGAACCGACCGACGTTGTCATCTCCTGAGCTAGTGTGAGAGGA 1076
Qy 361 GCTCTTGATTTCTTGCCCGCAGAGAGAGTCACTGAGTGAAGAGAGGCAACAGCTTCT 420
Db 1075 GCTCTTGATTTCTTGCCCGCAGAGAGAGTCACTGAGTGAAGAGAGGCAACAGCTTCT 1016
Qy 421 TAAAGCATCTGGATGGGTGAACCTTCAACAAGAAATTTGCTCACTTGTATCT 480
Db 1015 TAAAGCATCTGGATGGGTGAACCTTCAACAAGAAATTTGCTCACTTGTATCT 956
Qy 481 CAAGCCAGAAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTAT 540
Db 955 CAAGCCAGAAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTAT 896
Qy 541 TGACTTTGCTGGCTCAAGAAATGAAGATGAGATTGAATTTAAATTTTGGAGC 600
Db 895 TGACTTTGCTGGCTCAAGAAATGAAGATGAGATTGAATTTAAATTTTGGAGC 836
Qy 601 GCCGGAATTTGCTGCTCAAGAAATTTGAACTACGAGCCCTGGGTGGAAGCTGACAT 660
Db 835 GCCGGAATTTGCTGCTCAAGAAATTTGAACTACGAGCCCTGGGTGGAAGCTGACAT 776
Qy 661 GTGAGCATAGGCGTCACTACCTTACATCTCTTAAGTGGAGATTCCTTTCTGGAGGA 720
Db 775 GTGAGCATAGGCGTCACTACCTTACATCTCTTAAGTGGAGATTCCTTTCTGGAGGA 716
Qy 721 CACGAAGCAGAAAACATGGGAAATATACATCAGTGAATTACGACTTTGAAGAATTT 780
Db 715 CACGAAGCAGAAAACATGGGAAATATACATCAGTGAATTACGACTTTGAAGAATTT 656
Qy 781 CTTGAGCCATACGAGCGAGCTGGCCAGAGACTTTATTGGAAGCTTCTGTTAAAGAGAC 840
Db 655 CTTGAGCCATACGAGCGAGCTGGCCAGAGACTTTATTGGAAGCTTCTGTTAAAGAGAC 596
Qy 841 CCGGAAACGGCTCAACATCCAAAGAGCTCTAGACACCCCTGGATCAGCCGGTGGACAA 900
Db 595 CCGGAAACGGCTCAACATCCAAAGAGCTCTAGACACCCCTGGATCAGCCGGTGGACAA 536
Qy 901 CCAGCAAGCCATGGTGGACGAGAGTGTGTGTAATCTGAGAGAACTTCAGAGAGCACTA 960
Db 535 CCAGCAAGCCATGGTGGACGAGAGTGTGTGTAATCTGAGAGAACTTCAGAGAGCACTA 476
Qy 961 TGTCCGAGGCGGTGGAAGCTTTCTTCAGCATGCTGTCTCTGTGCAACAACCTCACCCG 1020
Db 475 TGTCCGAGGCGGTGGAAGCTTTCTTCAGCATGCTGTCTCTGTGCAACAACCTCACCCG 416

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OY 1021 CTCGCTGATGAAGAAGTGCACCTGAGGCGGATGATGAGACTGTGAGAGTGA 1080
Db 415 CTCGCTGATGAAGAAGTGCACCTGAGGCGGATGATGAGACTGTGAGAGTGA 356
OY 1081 CACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCGAGAGAGACAGACCTC 1140
Db 355 CACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCGAGAGAGAGACAGACCTC 296
OY 1141 CTAACCTGCTGACCTGACAGTGGCCGCGAGAGAGTGGGCGGAGGAGGCTCCCTTC 1200
Db 295 CTAACCTGCTGACCTGACAGTGGCCGCGAGAGAGTGGGCGGAGGAGGCTCCCTTC 236
OY 1201 GTGCAGA 1207
Db 235 GTGCAGA 229

RESULT 4
US-10-144-771-3361
; Sequence 3361, Application US/10144771
; GENERAL INFORMATION:
; APPLICATION: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 3361
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-3361

Query Match 59.3%; Score 1032.4; DB 8; Length 1732;
Best Local Similarity 83.8%; Pred. No. 2.3e-253;
Matches 1263; Conservative 0; Mismatches 186; Indels 59; Gaps 6;

OY 8 GCAGCTCAGGCTCCCGCCGATTTGATGTTCCAGGCTCAATGAGAGTCCAAACATGGAG 67
Db 91 GCAGCTCAGGCTCCCGCCGATTTGATGTTCCAGGCTCAATGAGAGTCCAAACATGGAG 150
OY 68 CCATTCAAGCAGAGAGTGGAGAGCTTTTATGACATCGAGAGAGAGCTGGGAGTGGC 127
Db 151 ACCTTCAAGCAGAGAGTGGAGAGCTTTTATGACATCGAGAGAGAGCTGGGAGTGGC 210
OY 128 CAGTTTGCATCTGAGAGAGTGCAGGAGAGAGCAGCGGCTTGAGTATGACAGCCAG 187
Db 211 CAGTTTGCATCTGAGAGAGTGCAGGAGAGAGCAGCGGCTTGAGTATGACAGCCAG 270
OY 188 TTCAATCAAGAGCGGAGAGCGGCGGAGCGGCGGCTGTGAGCCGAGAGAGATCGAG 247
Db 271 TTCAATCAAGAGCGGAGAGCGGCGGAGCGGCGGCTGTGAGCCGAGAGAGATCGAG 330
OY 248 CGGAGAGTGAAGATCTGCGGAGAGTGTGAGCAGCAATGTATCATACGCTGACAGCTC 307
Db 331 CGGAGAGTGAAGATCTGCGGAGAGTGTGAGCAGCAGCAATCATCATGCTGACAGCTC 390
OY 308 TATGAGAACCGGAGCGAGCTGTGTGACATCTTGAAGTATGTGTGTGAGAGAGAGCTCTC 367
Db 391 TATGAGAACCGGAGCGAGCTGTGTGACATCTTGAAGTATGTGTGTGAGAGAGAGCTCTC 450
OY 368 GATTTTCCGAGCCAGAGAGAGTCACTGAGTGAAGAGAGGCGCAGCAGCTTCATTAGCAG 427
Db 451 GATTTTCCGAGCCAGAGAGAGTCACTGAGTGAAGAGAGGCGCAGCAGCTTCATTAGCAG 510
OY 428 ATCTGTGATGGGTGAATACCTTCAACAAGAAATTTGCTCACTTTGATCTCAAGCA 487
Db 511 ATCTGTGATGGGTGAATACCTTCAACAAGAAATTTGCTCACTTTGATCTCAAGCA 570
OY 488 GAAAGATATATGTGTTAACAAGAAATTTCCATTCCACATCAAGCTGATGACTTT 547
Db 571 GAAAGATATATGTGTTAACAAGAAATTTCCATTCCACATCAAGCTGATGACTTT 630

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OY 548 GGTCTGCTACGAAATATGAAGATGAGATTGAATTTAAGATATTTTGGAGCCCGGAA 607
Db 631 GGTCTGCTACGAAATATGAAGATGAGATTGAATTTAAGATATTTTGGAGCCCGGAA 690
OY 608 TTTGTGTCTCCAGAAATTTGTAACTAGAGAGCCCTGGTCTGAGAGGCTGACATGTGAGC 667
Db 691 TTTGTGTCTCCAGAAATTTGTAACTAGAGAGCCCTGGTCTGAGAGGCTGACATGTGAGC 746
OY 668 ATAGGCTCATCACTCATCTCTTTAAGTGGAGATCCCTTTCCTGGAGACAGAG 727
Db 747 -----TCTAAGTGGAGGCTCCCTTCTCTGGAGACAGAG 783
OY 728 CAGAAACACTGCAATATATCATCAGTGAATTAAGACTTTGATGAGAGATTTCTTCAGC 787
Db 784 CAGAAACACTGCAATATATCATCAGTGAATTAAGACTTTGATGAGAGATTTCTTCAGC 843
OY 788 CATACAGAGAGCTGCGCAGAGCTTTATTCGGAAGCTTCTGTTAAAGAGACCGGAAA 847
Db 844 CATACAGAGAGCTGCGCAGAGCTTTATTCGGAAGCTTCTGTTAAAGAGACCGGAAA 903
OY 848 CGGCTCAATCCAGAGAGGCTCTCAGACACCCCTGATCAGCCGATGAGACCAAGCA 907
Db 904 CGGCTCAATCCAGAGAGGCTCTCAGACATCCCTGATCAGCCGATGAGACCAAGCA 963
OY 908 GCATGCTGCGAGCGGAGTCTGTGCAATCTGAGAACTTCAGAGAGAGAGATGTCCGC 967
Db 964 GCATGCTGCGAGCGGAGTCTGTGCAATCTGAGAACTTCAGAGAGAGAGATGTCCGC 1023
OY 968 AGCGGCTGAGAGCTTTCTTCAAGCATCGTGTCCCTGAGCAACCACTCAACGCTGCTG 1027
Db 1024 AGCGGCTGAGAGCTTTCTTCAAGCATCGTGTCCCTGAGCAACCACTCAACGCTGCTG 1083
OY 1028 ATGAAGAGTGAACCTGAGCGCGATGAGAGCTTGAAGAACTGTGAAGTGAATCTGAG 1087
Db 1084 ATGAAGAGTGAACCTGAGCGCGATGAGAGCTTGAAGAACTGTGAAGTGAATCTGAG 1143
OY 1088 GAGACATCTGCGAGAGAGAAAGCCCTCCACCGAGAGAGAGAGACACTCTTAATG 1147
Db 1144 GAGACATCTGCGAGAGAGAAAGCCCTCCACCGAGAGAGAGAGACTCTCTAATG 1203
OY 1148 GCCGACCTGAGAGGCGCGCAGAGAGTGTGAGCCAGCGGAGCTTCTGTGTGAGA 1207
Db 1204 GCCGACCTGAGAGGCGCGCAGAGAGTGTGAGCCAGCGGAGCTTCTGTGTGAGA 1260
OY 1208 CTTTGAACCCAGCTCAGACACAGACCCGAGCG-----TCTGAGAGACTTTGCAAG 1259
Db 1261 CTTTGAACCCAGCTCAGACATCAGATCCAGACATTCGTGTGTCTTGAAGACTTTGCAAG 1320
OY 1260 AGAGATGGGCCAGAGATTCAGAAAGAGCTTGACAGACAGCAGAGACCCCTGGAGCTG 1319
Db 1321 AGAGATGGGCCAGAGATTCAGAAAGAGCTTGACAGACAGCAGAGACCCCTGGAGCTG 1368
OY 1320 TGGCTGTCTTGTGTGAGAGAGCTTCAGACTTCCAAAGCTCTTAATTTCTCATTAATG 1379
Db 1369 TGGCTGTCTTGTGTGAGAGAGCTTCAGACTTCCAAAGCTCTTAATTTCTCATTAATG 1428
OY 1380 GCGTTTCTCTGTCTGCAATCTCAGAGTCTGGGGTGGAGAGTGAAGTTAGAGAAACAA 1439
Db 1429 GCGTTTCTCTGTCTGCAATCTCAGAGTCTGGGGTGGAGAGTGAAGTTAGAGAAACAA 1487
OY 1440 TTTAAAGAG-----CATCTCATATCAAGGGGTGAAGTCAAGTTAAGAGCCTT 1491
Db 1488 TTTCAAGAGTATCTTTTCTTTTAAACACAGGTAAAGGTAGATTAGGCGAGCTTT 1547
OY 1492 CTTCAAG 1499
Db 1548 CTTCAAG 1555

RESULT 5
US-09-947-907-15358/c
; Sequence 15358, Application US/09947907
; GENERAL INFORMATION:

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1  APPLICANT: IVENTER, J. Craig et al.
2  TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE
3  TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON EACH OF THE HUMAN
4  TITLE OF INVENTION: CHROMOSOMES. METHODS OF DETECTION, AND USES THEREOF
5  FILE REFERENCE: CL000896
6  CURRENT APPLICATION NUMBER: US/09/947, 907
7  CURRENT FILING DATE: 2003-03-17
8  PRIOR APPLICATION NUMBER: 60/241, 755
9  PRIOR FILING DATE: 2000-10-20
10 PRIOR APPLICATION NUMBER: 60/237, 768
11 PRIOR FILING DATE: 2000-10-03
12 PRIOR APPLICATION NUMBER: 60/231, 498
13 PRIOR FILING DATE: 2000-09-08
14 NUMBER OF SEQ ID NOS: 21266
15 SOFTWARE: fastSeq for Windows Version 4.0
16 SEQ ID NO 15358
17 LENGTH: 601
18 TYPE: DNA
19 ORGANISM: Human
20 US-09-947-907-15358

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Query Match      30.7%;   Score 534;   DB 5;   Length 601;
Best Local Similarity 99.6%;   Pred. No. 3,4e-126;
Matches 534;   Conservative 1;   Indels 0;   Gaps 0

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Db	GACTTTTGGACCCAGCTCAGCACCCGGGCGTCCTGAGACCTTTGCAAGAGAT	542

Db 541 GGGCCCAAGGAATTGAGAGAGCTTGCAGGCAAGCCAGAGAGCCCTGGAGCTGTGCTG 482

Db 481 TCTTCTGGGAGGAGGCTCCAGCATTTCCCAAGCTTTAATTCCTCATTAATAATGGGCTTT 422

1386 CCTCTGCTGCCAATCCTCAGAGCTTGGGGTGGGAGTGTGGACTTAGGAAAAACATATATA 1445  
 0Y  
 421 CCTCTGCTGCCAATCCTCAGAGCTTGGGGTGGGAGTGTGGACTTAGGAAAAACATATATA 362  
 Db

1446 GGCATCCCATCATATCACGGGGTGAAGGTCAGAGTAAGGCAGCCCTTCACACAGCTGAG 1505  
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Db 301 KGGGTTTCGAAACCGAGCTGGCCAAAAATTACACCGAGAGACAGAGTCTCCCCATTGGG 242

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RESULT 6  
US-09-949-016-1966  
; Sequence 1966, Application US/09949016

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1966
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1966

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Query Match	29.7%	Score 517.2	DB 51	Length 2157
Best Local Similarity	76.3%	Pred. No. 11e-121		
Matches 636; Conservative	0	Mismatches 198	Indels 0	Gaps 0

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61 CATGAGCATTTCAGCAGCAGAGAGGTGGAGACTTTATATGACATCGAGAGAGAGCTGGG 120  
145 CATGTCCAGTTTCAGGCGAGAGAGACGTGGAGGACCATTTATGACATGGGGGAGAGAGCTGGG 204

Db 205 CAGCGGCGCAGTTTGCATCGTGGGAGAGTCCCGGCAGAGGGCAGCGGSCAAGAGTAGCC 264

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 181 AGCAGATTCAATCAAGAAAGCGGAGAGACCGGGGAGAGCGCGGTGTGAGCCGGAGGA 240  
 265 AGCCAAATTCAATCAAGAAAGCGCGCTGTCAATCAGCGCGCGGTGTGAGCCGGAGGA 324

Db 325 GATCGAGCGGAGTGAAATCATCTGCGGAGATCCGGACCCCAATCATCATCCCTCA 384

Db 385 CGACATCTTCGAGAACAGACGAGACGTGTCCTCATCCTGTGAGCTGTCTCTGGCGGGGA 444

361 GCTCTTCGATTTCCTGCTCCAGAGAGAGTCACTGAGTGGAGGAGAGTCAACCACTTCAT 420  
 445 GCTCTTGACATTCCTGGGAGAGAGAGTCCGTGACGGAGGAGCGAGGGCCACCCAGTTCCT 504

421 TATGCAGATCTCTGGATGGGGTGAATCTTACACACAAAGAAATATGTCACATTTGATCT 480  
505 CAAGCAATCCCTGGACGGCGTTCACACTACTGCACTCTAAAGCCATCGCACACACTTTGACCT 564

D<sub>B</sub>  
601 CAGGCCGAAATTCATCTGTGGTCAAGAACAACCGAATCAGGCAT 624  
565 GAGCCGGAAAAATCATGCTGTGGAAGAAGAACATTTCCAATCCACATCAAGCATA 624

625 CGACTTCGGCATCGCGACAMGATCGAGCGCGGAGACGAGTTCAGACACATCTTCGGCAC 684

685 CCGGAGTTTGGCCCCAGAGATTGTGAACATATGAGCCGCTGGCCTTGAGAGCGGACAT 744

701 GAGGAGATACGGCTCACCACCACTCCATTAAAGCGAGAACACTTCTTTCTGAGAGA 720  
DB 745 GTGGAGCATCGGTGCATCACCTATAATCTCTTGAGGGGTGCATCCCCGTTTCCTGGGGGA 804

Db 805 GACCAAGAGGAGACGCTCACCAATCTCAGCCGTGACTACACTTCGACGAGGAGTA 864

Db 865 CTTGAGCAACACCGCGAGCTGSCCAAGACTTCATTGCGCGCTGCTGTCAAGATCC 924

Db 925 C A G C G G A G A T G A C C C A T T G C C C A G A G C C T G G A A C A T T C C T G A T T A A G G C G A T 978

RESULT 7  
US-60-443-566-467  
; Sequence 467, Application US/60443566  
; GENERAL INFORMATION:  
; APPLICANT: CARBELL, Michele  
; APPLICANT: BEGOVICH, Ann  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001447  
; CURRENT APPLICATION NUMBER: US/60/443,566  
; CURRENT FILING DATE: 2003-01-30  
; NUMBER OF SEQ ID NOS: 25102  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 467  
; LENGTH: 2201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-443-566-467

Query Match 29.7%; Score 517.2; DB 9; Length 2201;  
Best Local Similarity 76.3%; Pred. No. 1,1e-121;  
Matches 636; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

```
QY 61 CATGAGCCATTCAGCAGCAGAGAGTGGAGACTTTATGACATCGAGAGAGCTGGG 120
DB 189 CATGTCACGTTTCAGCAGCAGAGAGAGTGGAGACTTTATGAGATGGGAGAGCTGGG 248
QY 121 GATGCGCAGTTTCCATCGTGAAGATGCCGGAGAAAGACACGGGGCTTGAATATGC 180
DB 249 CAGCGGCCAGTTTGCATGTCGGAAGATGCCGGAGAAAGACACGGGGAGAGTACGC 308
QY 181 AGCCAAATTTCATCAGAAAGCGGAGACCGCGGAGACCGCGCGGTGTATGCGCGGAGAG 240
DB 309 AGCCAAATTTCATCAGAAAGCGGCGCTGTATCATCAGCCGCGGTGTATGCGCGGAGAG 368
QY 241 GATCGAGCGGAGAGTGAAGATCTCGCGGAGGAGTGTGACCAATATGTCATCAGCTGCA 300
DB 369 GATCGAGCGGAGAGTGAAGATCTCGCGGAGGAGTGTGACCAATATGTCATCAGCTGCA 428
QY 301 CGACGTCATAGAGAACCGACCGACGTCGTGACATCTTGAAGTATGTCTTGAAGAGAG 360
DB 429 CGACATCTTCAGAGAACAGACGTCGTGTCATCTGAGCTGTGTCTGTGCGGGGA 488
QY 361 GCTCTTCGATTTCTCGGCCAGAGAGTCACTGATGAGAGAGAGCCACAGCTTCAT 420
DB 489 GCTCTTCGATTTCTCGGCCAGAGAGTGTGTCGAGAGAGAGAGCCACAGCTTCCT 548
QY 421 TAAGCAGATCTCGATGGGGTGAATACCTTCAACAAAGAAATTTGCTCATCTTGTATCT 480
DB 549 CAAGCAGATCTCGAGCGGCTTCACTACCTGACCTTAAGCGCATGCGACATTTGACCT 608
QY 481 CAAGCAGAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTGAT 540
DB 609 GAAGCGGAGAAACATCATCTGCTGACAGAAAGTGCACCAACCAATCAAGCTCAT 668
QY 541 TGACTTTGCTGCTGCTCAACAATTAAGAGTGAATTTAAGATTTTTTGGAGC 600
DB 669 CGACTTCGAGATCGCGACAGAAATCGAGCGGGAGAAAGATTTCAAGAAATCTTCGCGAC 728
QY 601 GCCGGAATTTGTTGCTCCAGAAATTTGTAATCGAGCCCTGGTCTGAGGCTGACAT 660
DB 729 CCGGAGATTTGTGGCCCCAAGATTTGTAATGAGCGGCTGTGAGGCGGACAT 788
QY 661 GTGAGAGATAGGGCTCATCACTACCTCTTAAGTGAAGATCCCTTTCTGGGAGA 720
DB 789 GTGAGAGATAGGGCTCATCACTATATCTTCGAGCGGTCATCCCGTTCTGGGCGA 848
QY 721 CAGGAACAGAGAAACATGCGAAATATACATAGTGAAGTTAGACTTTGAGAGAT 780
DB 849 GACCAAGCAGAGAGAGCTCATCAACATCTGACCGGTAACTTGAAGTGAAGAGT 908
QY 781 CTTGAGCCATACGAGCAGCTGGCCAAAGAACTTTATTCGAGAGCTTGTGTTAAAGAC 840
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DB 909 CTTGAGCAACACCGAGAGCTGGCCAAAGACTTCATTCGCGGCTGCTCAAGATCC 968
QY 841 CCGGAACGCTCATCAATCCAAAGAGCTTCAGACACCCCTGATATACGCGCGT 894
DB 969 CAAGCGGAGAAATGCCATTCGCCAGAGCCCTGAACATTCCTGATTAAGCGCAT 1022
```

RESULT 8  
US-09-949-016-195  
; Sequence 195, Application US/09949016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 195  
; LENGTH: 2105  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-195

Query Match 29.6%; Score 515.6; DB 5; Length 2105;  
Best Local Similarity 76.1%; Pred. No. 2.8e-121;  
Matches 635; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

```
QY 61 CATGAGCCATTCAGCAGCAGAGAGTGGAGACTTTATGACATCGAGAGAGCTGGG 120
DB 93 CATGTCACGTTTCAGCAGCAGAGAGTGGAGACTTTATGATGAGTGGGAGAGCTGGG 152
QY 121 GATGCGCAGTTTCCATCGTGAAGATGCCGGAGAGAGACCGGGCTTGAATATGC 180
DB 153 CAGCGGCCAGTTTGCATGTCGGAAGATGCCGGAGAGAGAGAGAGAGAGAGTACGC 212
QY 181 AGCCAAATTTCATCAGAAAGCGGAGAGAGCGGCGAGAGCGCGGTGTGAGCCGGAGAG 240
DB 213 AGCCAAATTTCATCAGAAAGCGGCGCGCTGTATCCAGCGCGGTGTGAGCGGAGAG 272
QY 241 GATCGAGCGGAGAGTGAAGATCTCGCGGAGAGTGTGACCAATATGTCATCAGCTGCA 300
DB 273 GATCGAGCGGAGAGTGAAGATCTCGCGGAGATCGGAGACCCCAACATCATCCTTGCA 332
QY 301 CGACGTCATAGAGAACCGCACCGACGTGTGACATCTTGAAGTATGTCTGAGAGAG 360
DB 333 CGACATCTTCAGAGAACAGAGAGTGTGTCTTATCTTGAAGTGTCTTGTGGGGGA 392
QY 361 GCTCTTCGATTTCTCGGCCAGAGAGTCACTGAGTGAAGAGAGAGCCACAGCTTCAT 420
DB 393 GCTCTTCGATTTCTCGGCCAGAGAGTGTGTCTTATCTTGAAGTGTCTTGTGGGGGA 452
QY 421 TAAGCAGATCTCGATGGGGTGAATACCTTCAACAAGAAATTTGCTCATCTTGTATCT 480
DB 453 CAAGCAGATCTCGAGCGGCTTCACTACCTGACCTTAAGCGCATGCGACATTTGACCT 512
QY 481 CAAGCAGAAACATTAATGTTTGAACAAGAAATTTCCCATTCACACATCAAGCTGAT 540
DB 513 GAAGCGGAGAAACATCATCTGCTGAGCAAGAGCTGCCAACCAAGATTAAGCTCAT 572
QY 541 TGACTTTGCTGCTGCTCAACAATTAAGAGTGAATTTAAGATTTTTTGGAGC 600
DB 573 CGACTTCGAGATCGCGACAGATGAGAGCGGGAGAACAGTTCAAGAAATCTTGTGGGAC 632
QY 601 GCCGGAATTTGTTGCTCCAGAAATTTGTAATCGAGCCCTGGTCTGAGAGCTGACAT 660
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Db 633 CCGGAGTTTGTGCCCCAGAGATTGTAGCCGCTGGGCTGAGGCGGACAT 692
Qy 661 GTGAGCATATGAGCGCTCATCACTATACCTCTTAAAGAGCATCCCTTCTGGAGAG 720
Db 693 GTGAGCATATGAGCGCTCATCACTATACCTCTTAAAGAGCATCCCTTCTGGAGAG 752
Qy 721 CACGAGAGAGAACTCTGGCAATATATCATCACTAGTGAATTAAGAGATTT 780
Db 753 GACCAAGAGAGAGAGCTCACCAACATCTCAGCCGTGAATACGACTTGAAGAGAGTA 812
Qy 781 CTTGAGCATATGAGCGGAGCTGCGCAAGAGCTTTATTTGGAGAGCTTCTGGTTAAAGAGAC 840
Db 813 CTTGAGCAACACGAGCGAGCTGCGCAAGAGCTTATTTGCGGCTGCTGCAAGATCC 872
Qy 841 CCGGAAAGCGCTCATCACTCAAGAGCTCTGAGACACCCCTGAGTACGCGCGT 894
Db 873 CAAGCGAGATGACATTCCTCCAGAGCTTGAACATTTCTGATTAAGCGAT 926

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# RESULT 9

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PCT-US02-31357-118
; Sequence 118, Application PC/TUS0231357
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
; FILE REFERENCE: 21402-462D-061
; CURRENT APPLICATION NUMBER: PCT/US02/31357
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CirusSeqList version 0.1
; SEQ ID NO 118
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)..(1455)
PCT-US02-31357-118

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Query Match 29.6%; Score 515.6; DB 1; Length 2132;
Best Local Similarity 76.1%; Pred. No. 2.8e-121;
Matches 635; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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Qy 61 CATGAGCATTTCAAGCAGAGAGTGTAGAGACTTTTATGACATCGAGAGAGAGCTGGG 120
Db 93 CATGTCACGTTTACAGGAGAGAGAGTGTAGAGAGCATTATGAGAGAGAGAGAGCTGGG 152
Qy 121 GAGTGGCCAGTTTGGCATCTGGAAGAAGTCCCGGAGAGAGCAGCGGGCTTGAATATGC 180
Db 153 CAGGGCCAGTTTGGCATCTGCGGAGAGAGTCCCGGAGAGAGAGCAGGGCAGAGATAGCG 212

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Qy 181 AGCCAAATTTCATCAAGAGCGGAGAGCGCGGCGAGCCCGGCTGTAGCCGGAGGA 240
Db 213 AGCCAAATTTCATCAAGAGAGCGCGGCTGTATTCAGAGCGGCGGTGGAGGAGGAGGA 272
Qy 241 GATGAGGAGGAGGTGAGCATCTTCCGGCAGGTGTGTGACCAATATGATATACGCTTGA 300
Db 273 GATGAGGAGGAGGTGAGCATCTTCCGGGAGATCCGGACCCCAACATCATCACCTTGA 332
Qy 301 CGAGCTATATGAGAACCGGACCGAGTGTGACATCTTGAAGTATGAGTGTGAGAGGA 360
Db 333 CGACATCTTCAAGAACAGAGAGTGTCTTATCTTGAAGTGTGTCTTGGGGGGA 392
Qy 361 GCTCTTCATTTCTTGGCCGAGAGAGTCACTGAGTGAAGAGAGAGGACACAGCTTCAT 420
Db 393 GCTCTTGAATCTTCCGCGGAGAGAGAGTGTGTGACGAGAGAGAGAGGACACAGCTTCT 452
Qy 421 TAAGCATCTCTGAGTGGGGTGAACCTACCTTCAACAAGAAATTTGCTCATTTGATCT 480
Db 453 CAAGCAGATCTTGAACGGCTTCACTACCTGACCTTAAGGCGCATTCGACACTTTGACCT 512
Qy 481 CAAGCAGAAACATTTATGTTTGAACAAGATTTCCATTCACATCAAGCTGAT 540
Db 513 GAAGCGGAAACATTCATGCTGTGAGACAGAGCTGCCAACCAACATCAAGCTGAT 572
Qy 541 TGACTTTGCTGTGCTCAGAAATGAGATGAGTGAATTTAAGATATTTTGGAGC 600
Db 573 CGACTTGGGATTCGCGGACCAAGATGAGGCGGGAGAGAGATTCAGAAACATCTTCGGAC 632
Qy 601 GCCGAAATTTGCTCTCCAGAAATTTGAACTAGAGCCCTGGGCTGAGGCTGACAT 660
Db 633 CCGGAGTTTGTGCCCCAGAGATTGGAATGAGCCGCTGGGGCTGAGGCGGAGAT 692
Qy 661 GTGAGCATATGAGCGCTCATCACTATACCTCTTAAAGTGAACATCCCTTCTGGAGGA 720
Db 693 GTGAGCATATGAGCGCTCATCACTATACCTCTTAAAGTGAACATCCCTTCTGGAGGA 752
Qy 721 CACGAGAGAGAACTCTGCAATATCATCACTAGTGAATGAGTGTGAGAGATTT 780
Db 753 GACCAAGAGAGAGAGCTCATCAACATCTCAGCGGTGAACATCAAGCTTCAAGAGAGTA 812
Qy 781 CTTGAGCATATGAGCGGAGCTGCGCAAGAGCTTTATTTGGAAGCTTCTGTTAAAGAGAC 840
Db 813 CTTGAGCAACACGAGCGAGCTGCGCAAGAGCTTATTCGCGGCTGCTGCAAGATCC 872
Qy 841 CCGGAAAGCGCTCATCACTCAAGAGCTCTGAGACACCCCTGAGTACGCGCGT 894
Db 873 CAAGCGAGATGACATTCCTCCAGAGCTTGAACATTTCTGATTAAGCGAT 926

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# RESULT 10

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US-10-262-445-118
; Sequence 118, Application US/10262445
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catlett, Blina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Miller, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patunrajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan

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Db 372 CGACATCTTCAGAAACAAGAGAGTGTCTCTCCTGAGCTGTCTCTGGGCGGGA 431
Qy 361 GCTCTTCATTTCTGCGCCAGAAAGAGTCACTAGTGAAGGAGGCGACAGCTTCAT 420
Db 432 GCTCTTTCATCTCTGCGGAGAGAGTCTGTACGAGAGCGAGGCGCACCTGCTCT 491
Qy 421 TAAGCAGATCTGTGATGGGGTGAACCTACCTTCACAAAGAAATTTGCTCACTTGTATCT 480
Db 492 CAAGCAGATCTGTGAGCGGCTTCACTACCTGCACTTAAGGCACTGCACTTGTGACT 551
Qy 481 CAAGCAGAAACATTTATGTTGTTAGACAAGAAATTTCCATTCCACATCAAGCTGAT 540
Db 552 GAAGCGGAGAAACATCACTGTCTGTGACAGAACGTCGCCAACCAACATCAAGCTCAT 611
Qy 541 TGACTTTGCTGTGCTGCTCAAGAAATAGAGATGAGTTGAATTTAAGAAATTTTGGGAC 600
Db 612 CGACTTCGGCATCTGCGACAAAGATGAGCGGGAAACAGATTCAAGAAATCTTGGGAC 671
Qy 601 GCCGGAATTTGTGCTCCAGAAATTTGTAACCTACGAGCCCTGTGGTCTGAGGCTGACAT 660
Db 672 CCCGAGATTGTGTGCGCCAGAGATTGTGAATGAGCGCGCTGGGCTGTGAGGCGGACAT 731
Qy 661 GTGAGCATTAAGCGCTCATCATCTTACCTCTTAAAGTGAAGATCCCTTTCTGGGAGA 720
Db 732 GTGAGCATTCGGTGTCTATCATCTATATCTCTGTAGCGGTGATCCCGCTTCTGGGCGA 791
Qy 721 CACGAGAGAGAAACATCTGCGAAATATCATCATGATGATTACGCTTTGATGAGAAATT 780
Db 792 GACCAAGAGAGAGAGAGCTCACCAATCTCAGCCGTGAATCAAGCTTCAAGAGAGATA 851
Qy 781 CTTAGCATTATGAGAGAGAGTGTGCAAGAACTTTATTCGAAAGCTTCTGTTAAAGAGAC 840
Db 852 CTTAGCAACACAGCGAGAGCTGTGCAAGAACTTCTTGTGCGGCTGTCTGTCAAAAGATCC 911
Qy 841 CCGGAAACGGCTCACATTCAGAGGCTCTCAAGACCCCTGTGATCAG 889
Db 912 CAAGCGAGAAATGACATTCGCGCCAGAGCGCTGGAACATTCCTGATTAAG 960

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RESULT 12
US-09-724-676A-20895
; Sequence 20895, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20895
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-20895

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Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best Local Similarity 76.4%; Pred. No. 3.4e-121;
Matches 633; Conservativeness 0; Mismatches 196; Indels 0; Gaps 0;
Qy 61 CATGAGCATTCAAGCAGAGAGTGAAGACTTTATATGATCGAGAGAGCTGGG 120
Db 132 CATGTCACGTTCAAGCAGAGAGTGAAGACCATATATGATGAGGAGAGAGCTGGG 191

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Qy 121 GAGTGGCCAGTTTGGCATCTGTAAGAAAGTCCGGAGAGAGACAGGGCTTGAATATGC 180
Db 192 CAGCGGCGCAGTTTGGGATCTGTGGGAAGTGCCTGGGAGAAAGGACAGGGCAAGAGTACGC 251
Qy 181 AGCCAACTTCAATCAAGAGCGGCAAGAGCGGCGGAGCGGCTGTGAGCTGGGAGGA 240
Db 252 AGCCAACTTCAATCAAGAGCGGCGGCTGTGATCAAGCGGCGGAGGAGGACCGGAGGA 311
Qy 241 GATGAGCGGAGGAGATCTGTGCGGAGGTGTGTCACCAATGTATCATACGCTGCA 300
Db 312 GATGAGCGGAGGAGTGAATCTGTGCGGAGATCGGAGACCCCAATCATATCATCTTCA 371
Qy 301 CGAGCTTATAGAACCGCACAGAGCTGTGTCAATCTTGTAGTGTGTGAGAGGA 360
Db 372 CGACATCTTCAGAAACAAGAGAGTGTCTATCTGTGAGGCTGTCTGTGGGGGGA 431
Qy 361 GCTCTTCATTTCTGCGCCAGAAAGAGTCACTAGTGAAGAGGAGGACCAAGCTTCAT 420
Db 432 GCTCTTTCATCTCTGCGGAGAGAGTCTGTGACGAGAGACGAGGCGCACCACTTCT 491
Qy 421 TAAGCAGATCTGTGATGGGGTGAACCTACCTTCACAAAGAAATTTGCTCACTTGTATCT 480
Db 492 CAAGCAGATCTGTGAGCGGCTTCACTACCTGCACTTAAGGCACTGCACTTGTGACT 551
Qy 481 CAAGCAGAAACATTTATGTTGTTAGACAAGAAATTTCCATTCCACATCAAGCTGAT 540
Db 552 GAAGCGGAGAAACATCACTGTCTGTGACAGAACGTCGCCAACCAACATCAAGCTCAT 611
Qy 541 TGACTTTGCTGTGCTCAGAAATAGAGATGAGTTGAATTTAAGAAATTTTGGGAC 600
Db 612 CGACTTCGGCATCTGCGACAAAGATGAGCGGGAAACAGATTCAAGAAATCTTGGGAC 671
Qy 601 GCCGGAATTTGTGCTCCAGAAATTTGTAACCTACGAGCCCTGTGGTCTGAGGCTGACAT 660
Db 672 CCCGAGATTGTGTGCGCCAGAGATTGTGAATGAGCGCGCTGGGCTGTGAGGCGGACAT 731
Qy 661 GTGAGCATTAAGCGCTCATCATCTTACCTCTTAAAGTGAAGATCCCTTTCTGGGAGA 720
Db 732 GTGAGCATTCGGTGTCTATCATCTATATCTCTGTAGCGGTGATCCCGCTTCTGGGCGA 791
Qy 721 CACGAGAGAGAAACATCTGCGAAATATCATCATGATGATTACGCTTTGATGAGAAATT 780
Db 792 GACCAAGAGAGAGAGAGCTCACCAATCTCAGCCGTGAATCAAGCTTCAAGAGAGATA 851
Qy 781 CTTAGCATTATGAGAGAGAGTGTGCAAGAACTTTATTCGAAAGCTTCTGTTAAAGAGAC 840
Db 852 CTTAGCAACACAGCGAGAGCTGTGCAAGAACTTCTTGTGCGGCTGTCTGTCAAAAGATCC 911
Qy 841 CCGGAAACGGCTCACATTCAGAGGCTCTCAAGACCCCTGTGATCAG 889
Db 912 CAAGCGAGAAATGACATTCGCGCCAGAGAGCTGGAACATTCCTGATTAAG 960

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RESULT 13
US-09-724-676-20893
; Sequence 20893, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20893
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:

```



Qy 601 GCCGAAATTTGTCCTCCAGAAATTTGAACTACGAGCCCTGGCTGAGAGCTGACAT 660  
 Db 672 CCCGAGTTTGTGGCCCCAGAGATTGTGAACTATGAGCCGCTGGGCTGAGAGCGGACAT 731  
 Qy 661 GTGAGCATAGGCGCTCATCTACCTTACATCTCTTAAAGTGAGATCCCTTTCTTGGAGA 720  
 Db 732 GTGAGCATTCGGTGTCTATCCTTATCTCTGAGCGGTGATCCCGTTCCTGGGCGA 791  
 Qy 721 CACGAAGAGGAAACACTGGCAATATCATCATGAGTTACGACTTTGATGAGAAAT 780  
 Db 792 GACCAAGAGAGAGAGCTTCAACACATCTCAGCCGTAAGCTAGAGAGAGAGTA 851  
 Qy 781 CTTGAGCATAGAGAGAGCTGGCCCAAGACCTTTATTCGAAAGCTTCTGTTAAAGAGC 840  
 Db 852 CTTGAGCAACACAGAGAGCTGGCCCAAGACCTTATTCGCGGCTGCTGTGAAAGATCC 911  
 Qy 841 CCGGAAAGGCTCACATTCAGAGGCTCTCAGACACCCCTGGAT 885  
 Db 912 CAAGCGAAGATGACCATTTGCCAGAGCTTGAACATTCCTGAT 956

## RESULT 15

US-10-144-771-9285

; Sequence 9285, Application US/10144771

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF

; FILE REFERENCE: CU001321

; CURRENT APPLICATION NUMBER: US/10/144,771

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 47235

; SEQ ID NO 9285

; LENGTH: 1410

; TYPE: DNA

; ORGANISM: HUMAN

US-10-144-771-9285

Query Match 29.5%; Score 513.8; DB 8; Length 1410;

Best Local Similarity 76.2%; Pred. No. 6.9e-121;

Matches 632; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 61 CATGAGCCATTCAAGCAGACAGAGGTGAGACTTTTATGACATCGAGAGAGAGCTGG 120  
 Db 9 CATGTCACATTCAAGCAAGAGAGATTGTAGAGACATTATGATGAGAGAGAGACTTGG 68  
 Qy 121 GAGTGGCCAGTTTGCATCTGTGAAGAAGTGCAGGAGAAAGACGCGGCTTGAATATGC 180  
 Db 69 CAGTGGCCAAATTTGCCATCTGTGCGCAAGTGCAGAGAGGACGCGGCATGAGTATGC 128  
 Qy 181 AGCCAAGTTCAATCAAGAGCGGCAAGCGCGGCGGCGGCTGTGAGCCGGAGAGA 240  
 Db 129 AGCCAAGTTCAATCAAGAGCGGCGGCTGCATTCAGCGCGGCGGCTGTGAGCGGAGAGA 188  
 Qy 241 GATCAGCGGAGGTGAGCATCTCGGAGAGTGTGCAACAATGTCTATCAGCTGCA 300  
 Db 189 GATGGAAGCGAGGTGAGCATCTCGGAGAGTGTGCAACAATGTCTATCAGCTGCA 248  
 Qy 301 CGAGCTCTATGAAACCGACCGAGCTGTGACATCTTGAAGTATGTCTGAGAGAGA 360  
 Db 249 TGACCTGTTCGAAACAAGACAGATGTGTGATCTCTGAGAGTGTGTCCGTGGCGA 308  
 Qy 361 GCTCTTGATTTCCCTGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACAGCTTCA 420  
 Db 309 GCTTTTCATCTTCGGCCGAGAGAGAGTCACTGAGAGTGAAGGCCACAGCTTCT 368  
 Qy 421 TAAGCAGATCTGAGTGGGTGAATCTACCTTCAACAAGAAATTTGCTCACTTGTATCT 480  
 Db 369 CAABAATTCCTAGACGGGTCTCACTACTGCACTCCAAAGCGCATCGACACTTGAAGCT 428  
 Qy 481 CAAGCCAGAAAAATTAATGTGTGTGAGCAAGAATATTCATTCACATCAAGCTGAT 540  
 Db 429 GAAGCCGAGAAATCATGTGTGTGAGCAAGACGACGACGACCCCGCATTAAGCTCAT 488

Qy 541 TGACTTTGCTGCTCAGAAATAGAGATGAGTTGAATTTAAGAAATATTTTGGAGC 600  
 Db 489 CGACTTTGGCATTCGCGCACAGAGATGAGGCTGGCGAGATTCAAGAACATCTTTGGCAC 548  
 Qy 601 GCCGAAATTTGTGCTCCAGAAATTTGAACTACGAGCCCTGGTCTGAGAGCTGACAT 660  
 Db 549 ACCGAGTTTGTGCGCCCCGAGATGTGAATATGAGCACTTGGCTTGAAGCTGACAT 608  
 Qy 661 GTGAGCATAGGCGCTCATCTACCTTATCTCTTAAAGTGAGATCCCTTCTTGGGAGA 720  
 Db 609 GTGAGCATTTGCGCTCATCTACCTTATCTCTTAAAGTGAGATCCCTTCTTGGGAGA 668  
 Qy 721 CACGAAGAGGAAACACTGGCAATATCATCATGAGTTTACGACTTTGATGAGAAAT 780  
 Db 669 GACCAAGAGAGAGAGCTGAGAGACATCTCAGCACTGAATGATGAGAGAAAT 728  
 Qy 781 CTTGAGCATAGAGAGAGCTGGCCCAAGACTTTATTCGAAAGCTTCTGTTAAAGAGC 840  
 Db 729 CTTGAGCAGACACAGCGAGCTGGCCCAAGACTTCTATCCGAGGCTGTGTCAAGACCC 788  
 Qy 841 CCGGAAAGGCTCACATTCAGAGGCTCTCAGACACCCCTGGATCAG 889  
 Db 789 CAAGAGAGATGACCATTCGACAGAGCTTGAACATTCCTGATCAAG 837

Search completed: April 4, 2003, 22:50:26

Job time : 947.167 secs

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22 120 100.0 2235 25 US-09-649-163-9895 Sequence 9895, Ap
23 120 100.0 2235 25 US-09-652-917-3775 Sequence 3775, Ap
24 120 100.0 2235 27 US-09-698-010-12335 Sequence 12335, A
25 120 100.0 2235 27 US-09-698-013-6041 Sequence 6041, Ap
26 109 99.2 242 11 US-08-706-765-907 Sequence 907, App
27 109 99.2 362 13 US-08-975-985-2005 Sequence 2005, Ap
28 109 90.8 362 34 US-09-912-292-30021 Sequence 30021, A
29 106 88.3 362 34 US-09-912-292-30021 Sequence 3329, Ap
30 99.2 82.7 279 20 US-09-539-806-47575 Sequence 47575, A
31 97.6 81.3 1732 80 US-09-360-207-3361 Sequence 3361, Ap
32 85.6 71.3 422 27 US-09-698-010-6454 Sequence 6454, Ap
33 80.4 67.0 495 25 US-09-652-816-4516 Sequence 4516, Ap
34 80.4 67.0 495 25 US-09-652-816-4516 Sequence 137005,
35 79.4 66.2 434 19 US-09-528-409-88315 Sequence 88315, A
36 79.4 66.2 434 35 US-09-933-524-88315 Sequence 88315, A
37 79.4 66.2 434 35 US-09-933-524-88315 Sequence 88315, A
38 78.8 65.7 635 62 US-60-182-093-1080 Sequence 1080, Ap
39 78 65.0 377 21 US-09-540-766-53879 Sequence 53879, A
40 77.4 64.5 284 11 US-08-782-035-1455 Sequence 1455, Ap
41 77.4 64.5 284 21 US-08-782-035-1455 Sequence 37909, A
42 59 49.2 219 12 US-08-869-540-261 Sequence 261, App
43 59 49.2 219 45 US-60-018-911-261 Sequence 261, App
44 59 49.2 345 23 US-09-616-082-268 Sequence 268, App
45 58.4 48.7 332 18 US-09-411-587-970 Sequence 970, App
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## ALIGNMENTS

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RESULT 1
US-09-234-611-14012
; Sequence 14012, Application US/09234611
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/234,611
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14012
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-611-14012

Query Match 100.0%; Score 120; DB 16; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 60
DB 266 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 325

QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 120
DB 326 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 385

RESULT 2
US-09-235-076-19174
; Sequence 19174, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
```

```
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19174
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-19174
```

```
Query Match 100.0%; Score 120; DB 16; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 60
DB 266 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 325

QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 120
DB 326 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 385
```

```
RESULT 3
US-09-289-768-21173
; Sequence 21173, Application US/09289768
; GENERAL INFORMATION:
```

```
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21173
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-289-768-21173
```

```
Query Match 100.0%; Score 120; DB 16; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 60
DB 266 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGAGCACTGTGAGTGCAC 325

QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 120
DB 326 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGCAGCCTCC 385
```

```
RESULT 4
US-09-332-782-19174
; Sequence 19174, Application US/09332782A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/332,782A
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
/ SEQ ID NO 19174
/ LENGTH: 454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(454)
/ OTHER INFORMATION: n = A,T,C or G
US-09-332-782-19174
```

```
Query Match          100.0%; Score 120; DB 17; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 60
DB 266 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 325
QY 61 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGAGGAGGACACCTCC 120
DB 326 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 385
```

```
RESULT 5
US-09-737-223-19174
/ Sequence 19174, Application US/09737223
/ GENERAL INFORMATION:
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```
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/737,223
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 09/332,782
/ PRIOR FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19174
/ LENGTH: 454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(454)
/ OTHER INFORMATION: n = A,T,C or G
US-09-737-223-19174
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```
Query Match          100.0%; Score 120; DB 29; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 60
DB 266 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 325
QY 61 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 120
DB 326 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 385
```

```
RESULT 6
US-09-904-809-14012
/ Sequence 14012, Application US/09904809
/ GENERAL INFORMATION:
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```
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-757
/ CURRENT APPLICATION NUMBER: US/09/904,809
/ PRIOR FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: 09/234,611
/ PRIOR FILING DATE: 1999-01-22
/ NUMBER OF SEQ ID NOS: 21025
```

```
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 14012
/ LENGTH: 454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(454)
/ OTHER INFORMATION: n = A,T,C or G
US-09-904-809-14012
```

```
Query Match          100.0%; Score 120; DB 34; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 60
DB 266 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 325
QY 61 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 120
DB 326 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 385
```

```
RESULT 7
US-09-918-995-19174
/ Sequence 19174, Application US/09918995
/ GENERAL INFORMATION:
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```
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19174
/ LENGTH: 454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(454)
/ OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19174
```

```
Query Match          100.0%; Score 120; DB 34; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 60
DB 266 TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGACCTGAGGAAGCTGTGAGAGTGAC 325
QY 61 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 120
DB 326 ACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCCAGGAGGAGGAGGAGGACACCTCC 385
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```
RESULT 8
US-09-939-397-21173
/ Sequence 21173, Application US/09939397
/ GENERAL INFORMATION:
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```
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-765
/ CURRENT APPLICATION NUMBER: US/09/939,397
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 09/289,768
/ PRIOR FILING DATE: 1999-04-08
```

NUMBER OF SEQ ID NOS: 39996  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21173  
LENGTH: 454  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)...(454)  
OTHER INFORMATION: n = A,T,C or G  
US-09-939-397-21173

Query Match 100.0%; Score 120; DB 35; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1,7e-22;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 60  
DB 266 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 325  
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 120  
DB 326 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 385

RESULT 9  
US-09-757-982-12  
Sequence 12, Application US/09757982  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/757,982  
CURRENT FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: 09/163,115  
PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 480  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(480)  
US-09-757-982-12

Query Match 100.0%; Score 120; DB 29; Length 480;  
Best Local Similarity 100.0%; Pred. No. 1,7e-22;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 60  
DB 361 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 420  
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 120  
DB 421 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 480

RESULT 10  
PCT-US01-08631-9265  
Sequence 9265, Application PC/TUS0108631  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-049  
CURRENT APPLICATION NUMBER: PCT/US01/08631  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 9265  
LENGTH: 1253  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR  
LOCATION: (231)...(1250)  
OTHER INFORMATION: 100% homologous to Homo sapiens Death-associated protein kinase 2, accession number AB018001, Smith-Waterman Score=1732.  
PCT-US01-08631-9265

Query Match 100.0%; Score 120; DB 1; Length 1253;  
Best Local Similarity 100.0%; Pred. No. 2e-22;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 60  
DB 1131 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 1190  
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 120  
DB 1191 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 1250

RESULT 11  
US-09-277-214A-176  
Sequence 176, Application US/09277214A  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE  
FILE REFERENCE: NMI-079  
CURRENT APPLICATION NUMBER: US/09/277,214A  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 586  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 176  
LENGTH: 1451  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: All occurrences of n = any nucleotide  
US-09-277-214A-176

Query Match 100.0%; Score 120; DB 16; Length 1451;  
Best Local Similarity 100.0%; Pred. No. 2e-22;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 60  
DB 642 TCGCTGATGAAGAAGTGCACCTGAGCCGGATGAGACCTGAGAACTGTGAGGTGAC 701  
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 120  
DB 702 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGCAGCACTCC 761

RESULT 12  
US-09-891-825-176  
Sequence 176, Application US/09891825  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE  
FILE REFERENCE: NMI-079  
CURRENT APPLICATION NUMBER: US/09/891,825  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US/09/277,214  
PRIOR FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 586  
SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 176
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n = any nucleotide
US-09-891-825-176
```

```
Query Match          100.0%; Score 120; DB 33; Length 1451;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 60
DB 642 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 701
QY 61 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 120
DB 702 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 761
```

## RESULT 13

```
US-09-649-163-7647
; Sequence 7647, Application US/09649163
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Williamson, Mark
; APPLICANT: Richardson, Jennifer
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Villevial, Jean-Luc M.G.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: Slios-Santiago, Inmaculada
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; APPLICANT: Buefield, Samantha J.
; APPLICANT: Deedes, James
; APPLICANT: Lee, John
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1164-001
; CURRENT APPLICATION NUMBER: US/09/649,163
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/150,608
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 10535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7647
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-163-7647
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 60
DB 636 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 695
QY 61 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 120
```

```
DB 696 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 755
```

## RESULT 14

```
US-09-652-816-8022
; Sequence 8022, Application US/09652816
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1177-001
; CURRENT APPLICATION NUMBER: US/09/652,816
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,111
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9647
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8022
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-816-8022
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 60
DB 636 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 695
QY 61 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 120
DB 696 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 755
```

## RESULT 15

```
US-09-652-913-8169
; Sequence 8169, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Faib, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,107
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10813
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8169
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-8169
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 60
DB 636 TCGCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTTGAGAACTGTGAGAGTAC 695
QY 61 ACTGAGAGGACATCGCCAGAGAAAGCCCTCCACCCACGAGAGAGAGACGACACTCC 120
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Db 696 ACTGAGAGSACATCGCCAGAGAGAAAGCCCTCCACCCACGAGGAGGAGCAGCACTCC 755

Search completed: April 4, 2003, 22:30:07  
Job time : 372.763 secs

ORGANISM: HOMO S

Query Match 100.0%; Score 120; DB 6; Length 1442;  
Best Local Similarity 100.0%; Pred. No. 1.8e-24;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 60  
Db 414 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 355

Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 120  
Db 354 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 295

RESULT 3  
US-60-443-566-647  
Sequence 647, Application US/60443566  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
APPLICANT: BEGOVICH, Ann  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001447  
CURRENT APPLICATION NUMBER: US/60/443,566  
CURRENT FILING DATE: 2003-01-30  
NUMBER OF SEQ ID NOS: 25102  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 647  
LENGTH: 2085  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-60-443-566-647

Query Match 100.0%; Score 120; DB 9; Length 2085;  
Best Local Similarity 100.0%; Pred. No. 1.9e-24;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 60  
Db 1029 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 1088

Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 120  
Db 1089 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 1148

RESULT 4  
US-09-539-806B-47575  
Sequence 47575, Application US/09539806B  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaby, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE  
FILE REFERENCE: PD-1027 CIP  
CURRENT APPLICATION NUMBER: US/09/539,806B  
CURRENT FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: 08/706,766  
PRIOR FILING DATE: September 27, 1996  
PRIOR APPLICATION NUMBER: 60/004,676  
PRIOR FILING DATE: October 2, 1995  
PRIOR APPLICATION NUMBER: 08/749,515  
PRIOR FILING DATE: November 15, 1996  
PRIOR APPLICATION NUMBER: 60/006,810  
PRIOR FILING DATE: November 15, 1995  
PRIOR APPLICATION NUMBER: 08/822,285  
PRIOR FILING DATE: March 20, 1997  
PRIOR APPLICATION NUMBER: 60/013,696  
PRIOR FILING DATE: March 20, 1996  
PRIOR APPLICATION NUMBER: 08/951,197  
PRIOR FILING DATE: October 1, 1997

PRIOR APPLICATION NUMBER: 60/027,249  
PRIOR FILING DATE: October 1, 1996  
PRIOR APPLICATION NUMBER: 08/826,438  
PRIOR FILING DATE: March 20, 1997  
PRIOR APPLICATION NUMBER: 60/016,145  
PRIOR FILING DATE: April 18, 1996  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 48372  
SOFTWARE: PERL Program  
SEQ ID NO 47575  
LENGTH: 279  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Inctye ID No: rat0065778  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 9  
OTHER INFORMATION: a, t, c, g, or other  
US-09-539-806B-47575

Query Match 82.7%; Score 99.2; DB 5; Length 279;  
Best Local Similarity 89.2%; Pred. No. 9.9e-19;  
Matches 107; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 60  
Db 76 TCGCTGATGAAGAAGTGCACCTTGAGCACTTGAGCACTTGAGAACTGTGAGAGTAC 135

Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 120  
Db 136 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 195

RESULT 5  
US-10-144-771-3361  
Sequence 3361, Application US/10144771  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig  
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
FILE REFERENCE: C1001321  
CURRENT APPLICATION NUMBER: US/10/144,771  
CURRENT FILING DATE: 2002-05-15  
NUMBER OF SEQ ID NOS: 47235  
SEQ ID NO 3361  
LENGTH: 1732  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-144-771-3361

Query Match 81.3%; Score 97.6; DB 8; Length 1732;  
Best Local Similarity 88.3%; Pred. No. 4e-18;  
Matches 106; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGCACCTTGAGCCGCGATGAGACCTTGAGAACTGTGAGAGTAC 60  
Db 1078 TCGCTGATGAAGAAGTGCACCTTGAGCACTTGAGCACTTGAGAACTGTGAGAGTAC 1137

Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 120  
Db 1138 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCCGAGGAGAGGAGGACGACCTCC 1197

RESULT 6  
US-10-338-044-386/c  
Sequence 386, Application US/10338044  
GENERAL INFORMATION:  
APPLICANT: MENDRICK, Donna  
APPLICANT: PORTER, Mark  
APPLICANT: JOHNSON, Kory  
APPLICANT: HIGGS, Brandon  
APPLICANT: CASTLE, Arthur



```

1  APPLICANT: ELASHOFF, Michael
2  TITLE OF INVENTION: Molecular Cardiototoxicology Modeling
3  FILE REFERENCE: 44971-8090-01-US
4  CURRENT APPLICATION NUMBER: US/10/338.044
5  CURRENT FILING DATE: 2003-01-27
6  PRIOR APPLICATION NUMBER: US 60/303,819
7  PRIOR FILING DATE: 2001-07-10
8  PRIOR APPLICATION NUMBER: US 60/305,623
9  PRIOR FILING DATE: 2001-07-17
10 PRIOR APPLICATION NUMBER: US 60/369,351
11 PRIOR FILING DATE: 2002-04-03
12 PRIOR APPLICATION NUMBER: US 60/377,611
13 PRIOR FILING DATE: 2002-05-06
14 NUMBER OF SEQ ID NOS: 2696
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 386
17 LENGTH: 649
18 TYPE: DNA
19 ORGANISM: Rattus norvegicus
20 FEATURE:
21 OTHER INFORMATION: Genbank Accession No. AB692388
22 US-10-338-044-386

```

Query Match	80.7%	Score 96.8	DB 8	Length 649
Best Local Similarity	89.7%	Pred. No. 5.6e-18		
Matches 104	Conservative	0	Mismatches 12	Indels 0
			Gaps	0

OY 5 TGAAGAAAGGTGCACTGAGGCCGATGTAGAGACCTGGAGATCACTG 64  
 Db 649 TCAATGAAGAGTGCCTTGAAGACATGAGACTGTGAGAACTCCAGATGACACGG 590  
 OY 65 AGAGAGACATGCGCCAGAGAAAGCCCTCCACCGAGAGAGAGACGACCTCC 120  
 Db 589 AGGAGAACATTGCCAGAGAAAGCCCTTACCCCCGGAGAGAGACGATCTCC 534

```

RESULT 7
US-09-947-907-15359/c
; Sequence 15359, Application US/09947907
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISM (CSNPS) LOCATED ON EACH OF THE HUMANH2B PROTEIN
; TITLE OF INVENTION: CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CLO00896
; CURRENT APPLICATION NUMBER: US/09/947, 907
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 21266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15359
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-947-907-15359

```

Query Match	57.0%	Score	80.4	DB 5	Length	601	
Best Local Similarity	98.8%	Pred. No.	2.4e-13				
Matches	81	Conservative	0	Mismatches	0	Gaps	0

Qy 39 CCTAGGAACTGTGAGACTGACACTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCC 98  
|||  
Db 422 CCAGGGAATGTGAGAGTGACCTGAGGAGGACATCGCCAGAGGAAAGCCCTCCACCC 363

QY 99 ACGAGGAGGAGCAGCACCCTCC 120  
|||  
Db 362 ACGAGGAGGAGCAGCACCCTCC 341

RESULT 8  
PCT-US03-01096-36  
; Sequence 36, Application PC/TUS0301096  
; Error: TUS0301096

```

1  APPLICANT: INCYTE GENOMICS, INC.; JONES, Anilasa L.;
2  APPLICANT: DAHL, Christopher R.; GIEZTEN, Darryl;
3  APPLICANT: CHINN, Joyce; DUFOUR, Gerard B.;
4  APPLICANT: JACKSON, Jennifer L.; YU, Jimmy Y.;
5  APPLICANT: TUSON, Olivia; YAP, Pierre S.;
6  APPLICANT: AMSHEY, Stefan R.; DAM, Tam C.;
7  APPLICANT: LIU, Tommy F.; GERSTIN Jr., Edward H.;
8  APPLICANT: PERALTA, Careyna H.; LEWIS, Samantha A.;
9  APPLICANT: CHEN, Alice; MAKAWA, Rakesh;
10 APPLICANT: LAM, Ruth Y.; UNASHKA, Michael;
11 APPLICANT: R., KRISHNAN, Seenivasara R.; KOLLURU, Vijaykumar;
12 APPLICANT: PANESAR, Iqbal S.
13
14 TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
15
16 FILE REFERENCE: PT-1239 PCT
17
18 CURRENT APPLICATION NUMBER: PCT/US03/01096
19
20 PRIOR FILING DATE: 2003-01-13
21
22 PRIOR APPLICATION NUMBER: US 60/349,384
23
24 PRIOR FILING DATE: 2002-01-16
25
26 PRIOR APPLICATION NUMBER: US 60/349,946
27
28 PRIOR FILING DATE: 2002-01-17
29
30 PRIOR APPLICATION NUMBER: US 60/349,413
31
32 PRIOR FILING DATE: 2002-01-17
33
34 NUMBER OF SEQ ID NOS: 377
35
36 SOFTWARE: PERL Program
37
38 SEQ ID NO 36
39
40 LENGTH: 1195
41
42 TYPE: DNA
43
44 ORGANISM: Homo sapiens
45
46 FEATURE:
47
48 NAME/KEY: misc feature
49
50 OTHER INFORMATION: Incyte ID No: LG:7761755.9;2002JAN18
51
52 PCT-US03-01096-36

```

Query Match	67.0%	Score 80.4	DB 1	Length 1195
Best Local Similarity	99.8%	Pred. No. 2.8e-13		
Matches 81	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 39	CCTGAGAACTGTGAGATGACACTGAGAGAGACATGCCACGAGAGAAAGCCCTCCACC	98		
Db 914	CCAGGAGCACTGTGAGATGACACTGAGAGAGACATGCCACGAGAGAAAGCCCTCCACC	973		
Qy 99	ACGGAGGAGGAGCAGCACTCC	120		
Db 974	ACGGAGGAGGAGCAGCACTCC	995		

```

RESULT 9
US-60-443-566-10041
; Sequence 10041, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C10014447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ. ID NOS: 25102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10041
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-443-566-10041

```

Query Match	50.8%	Score 61	DB 9	Length 201
Best Local Similarity	100.0%	Pred. No.	6.2e-08	
Matches 61	Conservative 0	Mismatches 0	Indels 0	Gaps 0

**QY** 60 CACTGAGGAGCATCGCCAGGAGGAAAACCTTCACCCACGGAGGAGGACACCTC 119  
| | | | |  
**Db** 1 CACTGAGGAGCATCGCCAGGAGGAAAACCTTCACCCACGGAGGAGGACACCTC 60

QY	120	C	12
Db	61	C	61

RESULT 10  
US-10-266-131-2686

OTHER INFORMATION: n = A, T, C or G  
US-10-266-131-2686

QY 61 ACTGAGG 67  
| | | | |  
Db 603 ACAGAGG 609

```

RESULT 11
US-10-388-360-334/C
Sequence 334, Application US/10388360
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH
APPLICANT: Baker, Joffe B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kiefer, Michael C.
APPLICANT: Shak, Steve
APPLICANT: Walker, Michael Graham
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPRIED TUMOR TISSUES
FILE REFERENCE: 39740-0001US
CURRENT APPLICATION NUMBER: US/10/388,360
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 384
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 334
LENGTH: 3373

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-334

```

Query Match	27.8%	Score 33.4	DB 7	Length 3373
Best Local Similarity	57.0%	Pred. No. 7.2		
Matches 61; Conservative	0	Mismatches	46	Indels 0; Gaps 0

QY 67 GAGGACATCGCCAGGAGGAAAGCCCTCCACCCACGAGGAGGAGCAG 111  
Db 55 GGTGCCGAGGGAGGAGGAGGAGGCCGCTCCCGGCGCAGAGGAGGAAG 9

```

RESULT 12 257-1083/c
US-10-264-237-1083/c
Sequence 1083, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Bire et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P133P1
CURRENT APPLICATION NUMBER: US/10/264,237
PCT FILING DATE: 2002-10-04
PRIORITY APPLICATION NUMBER: PCT/US01/16450
PRIORITY FILING DATE: 2001-05-18
PRIORITY APPLICATION NUMBER: US 60/205,515
PRIORITY FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1083
LENGTH: 595
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (551)..(551)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (575)..(575)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (577)..(577)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (587)..(587)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1083

```

Query March	26.8%	Score 32.2;	DB 8;	Length 595;
Best Local Similarity	63.6%;	Pred. No. 1;		
Matches 49;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0;

QY 104 GGAGGAGCAGCACCCTCC 120  
Db 403 GGATGAGCGGCTCCTTC 387

RESULT 13  
US-60-452-680-6448/C  
; Sequence 6448, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: GRUPE, Andrew



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